Title:

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1789
1 MLQKPKSVKLRALRSPRKEG.....SRIYKPQTRLKRKQPVRKRQ 338
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                                             P56201 oryctolagus
P2323 xenopus lae
P12502 sinian immu
P12503 human immun
P17757 human immun
P01029 mus musculu
P18042 human immun
P42487 african swi
O00273 homo sapien
O74454 schizosacch
O95613 homo sapien
O9uhd4 homo sapien
O9uhd4 homo sapien
O60543 homo sapien
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bos taurus
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Result

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α.	83.5	84	84	84	84.5	84.5	84.5	85.5	85.5	85.5	86
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P87138 schizosacch	P56198 mus musculu	P41571 ceratitis c					Q39057 arabidopsis			mus	

ALIGNMENTS

CC condensation during apoptosis. Degrades naked DNA and induces CC apoptotic morphology.	000-
"Structure a fragmentatic neuroblastom	
Nakagawara A. Submitted (JU	
RP SEQUENCE FROM N.A. (ISOFORMS BETA; GAMMA AND DELTA). RC TISSUE-Fetal brain;	
Curr.	-
"CPAN, a	
RA <u>Halenbeck R.</u> MacDonald H., Roulston A., Chen T.T., Conroy L., RA <u>Williams T.T.</u>	J
TISSUE-Pancreas;	a .a .
FROM N A	
DNage.";	
Nagata S.; "Molecular cloning and characterization of human	
RA Mukae N., Enari M., Sakahira H., Fukuda Y., Inazawa J., Toh H.,	
[2]	
fragmentation and chromatin condensation during apoptosi proc. Natl. Acad. Sci. U.S.A. 95:8461-8466(1998)	
Liu X., Li P., Wid	_,]
NCBI_TaxID=9606; [1]	m C
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	· ·
DFFB OR DFF2 OR DFF40 OR CAD. Homo sapiens (Human).	~ ~
DE (Caspase-activated deoxyribonuclease) (Caspase-activated DNase) (CAD) DE (Caspase-activated nuclease) (CPAN).	
DNA fragmentation factor 40 kDa subunit (EC 3) (DFF-40)	
16-OCT-2001 (Rel. 40, Last sequence upd	
076075; 060521; Q9BYI4; Q9BYI5; Q9BYI	٠.
DFFB_HUMAN STANDARD; PRT; 338 AA.	
RESULT 1	-

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EMBL; AB013918; BAA32250.1; --
EMBL; AF039210; AAC39709.1; --
EMBL; AF028911; BAB40447.1; --
EMBL; AB028911; BAB40448.1; --
EMBL; AB028913; BAB40449.1; --
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HSSP; C
Genew;
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DOMAIN
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SUBUNIT: HETERODIMER OF A 45 kDa AND A 40 kDa SUBUNIT.
SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
ALTERNATIVE PRODUCTS: 4 isoforms; Alpha (shown here), Beta, and Delta; are produced by alternative splicing.
SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                    241
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       301
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                              LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS 240
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                                                                                                                              INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300
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                                                                                                                                                                                                   EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                                                                                                                                                                                     DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA
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                                                                                                 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
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IPR003508; CAD.
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GVLLCGPG (IN ISOFORM BETA).
YVSDIRRELSAFHEPQVGLIQAAQOLLCDEOAPQRQ ->
VGVRARTKTRDTSSLSPGDCQALGNGGRCGQRLFL (IN
YCVSDRM GAMMA).
MISSING (IN ISOFORM GAMMA).
YVSDIRRELSAFHEPQVGLIQAA -> WFCHVSQDSLTLL
YVSDIRRELSAFHEPQVGLIQAA -> WFCHVSQDSLTLL
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Pred. No. 5.3e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Casp...
DFFB OR CAD.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; Metazoa; Rodentia; Motazoa; Rodentia;
                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease; Nuclear protein; Apoptosis DOMAIN 7 83 CIDE-N. SEQUENCE 344 AA; 39449 MW; E854B413EA139DE1
                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1196287; Dffb.
InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98082976; PubMed-9422513;
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15-JUN-2002 (Rel. 41, Last annotation update)
DNA fragmentation factor 40 kDa subunit (EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 391:43-50(1998). 缼
                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic and SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptotic morphology.
ENZYME REGULATION: Inhibited by DFFA (DFF45).
SUBUNIT: HETERODIMER OF A 45 kDa AND A 40 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Nuclease that induces DNA fragmentation condensation during apoptosis. Degrades naked DNA
184
                             181
                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                           124
                                                                                                                      64
                                                                                                                                                                                                                                            261;
                                                                                                                                                                                 4
                                                                                                                                                                                                             1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                         Similarity
               EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                         DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA
                                                                                                                                                  PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA
                                                                                                                                                                            VLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCF
AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                                         DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYTSMVDE
                                                                                                                    PGLPNDAELLLLTAGETWHGYVSDITRFLSVFNEPHAGVIQAARQLLSDEQAPLRQKLLA
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              institutions as long as its content
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77.2%;
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                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                         Score 1416; DB 1;
Pred. No. 8.2e-115;
37; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                    E854B413EA139DE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degrades DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344
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                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT
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; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21319171; PubMed-11425895;
Cao G., Pei W., Lan J., Stetler R.A., Luo Y., Nagayama T.,
Graham S.H., Yin X.M., Simon R.P., Chen J.;
Caspase-activated DNase/DNA fragmentation factor 40 mediates
apoptotic DNA fragmentation in transient cerebral ischemia and in
neuronal cultures.",
J. Neurosci. 21:4678-4690(2001).
J. Neurosci. 21:4678-4690(2001).
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15-JUN-2002 (Rel. 41, Last annotation update)
DNA fragmentation factor 40 kDa subunit (EC 3.----) (DFF-40)
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1: ENVYME REGULATION. Inhibited by DFFA (DFF45).
-1- SUBGUNIT: HETERODIMER OF A 45 KDA AND A 40 KDA SUBGUNIT.
-1- SUBCELLGLAR LOCATION: Cytoplasmic and nuclear (By similarity).
-1- SIMILARITY: CONTAINS 1 CIDE N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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15-JUN-2002
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                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptotic morphology.
ENZYME REGULATION: Inl
SUBUNIT: HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condensation during apoptosis. Degrades naked
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                                 121 DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180
                                                                                                                                                                                                                                  257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             norvegicus (Rat).
                                                                                                                                                                                                                                                    Similarity
DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYISMVDA
                                                                                                                                                    VLPQPKCVKLRALHSSCKFGVAARSCQELLRKGCIRFQLPVPGSRLCMYEDGTEVTDDCF 63
                                                                                                                                                                                        MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                          PSLPNDSELLLTAGETWHGYVSDITRLLSVFNEPHAGVIQAARQLLSDEQAPLRQKLLA 123
                                                                                                             PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120
                                                                                                                                                                                                                                                                                                                                                Nuclease;
                                                                                                                                                                                                                                                                                                            349 AA;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deoxyribonuclease) (Caspase-activated DNase) (CAD).
                                                                                                                                                                                                                                                                                                        40096 MW;
                                                                                                                                                                                                                                                  77.8%;
                                                                                                                                                                                                                                                                                                                            Nuclear protein; Apoptosis.
                                                                                                                                                                                            red. No. 9.9e-113; 38; Mismatches 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     induces DNA fragmentation and chromat ptosis. Degrades naked DNA and induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                          F125972A110FE398 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996
01-FEB-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: INTEGRAL COMPONENT OF THE FILAMENTOUS MATRIX OF THE CENTROSOME INVOLVED IN THE INITIAL ESTABLISHMENT OF ORGANIZED MICROTUBBLIE ARRAYS IN BOTH MITOSIS AND MEJOSIS.
-I- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN KIDNEY, THYMUS AND LIVER. LOW LEVELS IN BRAIN, MUSCLE, LUNG AND HEART.
-I- DOMALN: COMPOSED OF A COILED-COIL CENTRAL REGION FLANKED BY NON-HELICAL N- AND C-TERMINALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microtubule organization.";
Cell 76:639-650(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCNT_MOUSE
P48725;
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pericentrin PCNT.
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: STRONG, TO HUMAN KENDRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxsey S.J., Stein P., Evans L., Calarco P.D., Kirschner M., Pericentrin, a highly conserved centrosome protein involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94170365; PubMed=8124707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                 Local
                                                                                                                  142
                                                                                                                                                                                                                                                                                                                                # U05823; AAA17886.1; -.
# MGI:102722; Pcnt.
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108 CDEQAPQRQLL-----ADLLHNVSQNIAA-----ETRAEDPPWFEGLESRFQSKSG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AAREEYLRVLSSMCHKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                               198 AAELKEKLRSEMEKNAQ-TIETLKQDWESERELCLENLRQELSLKHQSEMEGLQSQFQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                               2 LOKPKSVKLRALRSPRKFGVAGRSCQEVL----RKGC----LRFQLPERGSRLCLY--ED
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                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEODGREVDWEYFYGLLFTSENLK 300
                                                                                GTELTEDYFPSVPDNAELVLLTLGQAWQG----YVSDIRRFLSAFHEPQVGLIQAAQQLL 107
                                                                                                                 LQKEKETALTELREM----LNGRRAQELALLQSRQQCELELLREQHAREKEEMALRSGQE 197
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                                                                                                                                                                                                                                                 1920 AA;
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(Rel. 33,
(Rel. 39,
                                                                                                                                                                                                                                                                                  110
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                Microtubules.
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                                                                                                                                                                                                                                                 218337 MW;
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Last sequence up
Last annotation
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Pred. No. 0.
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                                                                                                                                                                                                                                                 CF1D0ADEC5B73309 CRC64;
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                                                                                                                                                                                                                DB 1;
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RESULT 5
VIME_MOUSE
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P20152; 008704;
01-FEB-1991 (Rel: 1
01-MAY-1992 (Rel: 2
15-JUN-2002 (Rel: 4
                                                                                                                                                                                                        "Transcriptional regulation myeloid leukemia M1 cells."; Gene 166:281-286(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Spleen;
Prvstowsky M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-89306653;
          Ando S., Tokui T., Yamauchi T., Sugiura H., Tanabe K., "Evidence that Ser-82 is a unique phosphorylation site for Ca2(+)-calmodulin-dependent protein kinase II."; Biochem. Biophys. Res. Commun. 175:955-962(1991).
                                                                                                                                                                                                                                                                                                                                                                 Capetanaki Y., Kuisk I., Rotnorum R., Constant of the viscous vimentin: structural relationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90220517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood L., Theriault N., Vogeli G.;
"Vimentin cDNA clones covering the
protein are found in an EHS tumor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                     using preparative two-dimensional Electrophoresis 15:735-745(1994).
                                                                                                             Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
                                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to
                                                                                                                                                                                                                                                                                                                                                               Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood L., Theriault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                MEDLINE-91222208; PubMed-1850997;
                                                                             PHOSPHORYLATION OF
                                                                                                                                                                    TISSUE-Fibroblast;
                                                                                                                                                                                 SEQUENCE OF 71-90.
                                                                                                                                                                                                                                               Nakamura N., Shida M.,
                                                                                                                                                                                                                                                           MEDLINE-96125204;
                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90265604; PubMed-2140597;
Capetanaki Y., Kuisk I., Rothblum
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90220517; PubMed-2325630;
Hennekes H., Kuehn S., Traub P.;
"Coding sequence and flanking regions
Mol. Gen. Genet. 221:33-36(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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  FUNCTION:
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Rodentia;
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PIR; S12774;
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PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS C
MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
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M26251;
Z22526;
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Y07738;
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1038; filament; 1.
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20.1%;
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SEQUENCE FROM N.A.
MEDLINE-83297272; PubMed=6688458;
Bloemendal H., Quax W., Quax-Jeuken Y., Dodemont H., Ramaekers
Bloemendal H., Quax W., Dunia I., Benedetti L.;
Dunia I., Benedetti L.;
"Organization and expression of the vimentin gene.";
Mol. Biol. Rep. 9:115-118(1983).
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01-FEB-1996
15-JUN-2002
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EMBL; X87227; CAA60679.1; -.
InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

'I FUNCTION: Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells.

'I SUBURT: HOMODILYMER

'I PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS OF MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY REORGANIZED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; Cricetulus.
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162 EDIIR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI- 213
                                 27
                                                                    63;
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                               QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
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Pred. No. 0.
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                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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21-JUL-1986
15-JUN-2002
EMBL; K00927; AAA37104.1;
EMBL; K00921; AAA37104.1;
EMBL; K00922; AAA37104.1;
EMBL; K00923; AAA37104.1;
EMBL; K00924; AAA37104.1;
                                                                                                                                                                                                                                                                                                                                                   MEDIINE-83221633; PubMed-6304716;
Quax-Jeuken Y.E.F.M., Quax W.J., Bloemendal H.;
"Primary and secondary structure of hamster vimentin predicted from
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The structure of the vimentin gene."; Cell 35:215-223(1983).
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Bloemendal H.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=10036;
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P02544;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    SUBURIT: HOMOPOLYMER.

PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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                                                                                                                                                                                                                           EORGANIZED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
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(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
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MEDLINE-92171936; PubMed-1540169;
Bussemakers M.J.G., Verhaegh G.W.
                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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01-JUL-1993
15-JUN-2002
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EMBL; K00926; AAA37104.1;
PIR; A02959; VEHY
                       SEQUENCE FROM N.A.
                                                            Rattus norvegicus
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Pfam; PF00038; filament;
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LINKER 1.
COIL 1B.
LINKER 12.
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Pred. No.
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7; Mismatches
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COSTA 2.
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PHOSPHORYLATION (BY CAMK2)
SIMILARITY).
PHOSPHORYLATION (BY CAMK2)
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                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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-> D (IN REF. 2).
-> I (IN REF. 2).
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Submitted (
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EMBL; X62952; CAA44722.1; -. EMBL; M84481; AAA42339.1; -.
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PIR; JQ1389; JQ1389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 85-159 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001664; IF. Pfam; PF00038; filament; PR05ITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Various non-epithelial cells, especially mesenchymal cells SUBUNIT: HOMOPOLYMER.

FIN: HOMOPOLYMER.

FIN: HOMOPOLYMER.

FIN: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CEL
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
KMALDIEIATYRKLL----EGEESRISLPLPNFSSLNLRETNLESLPLVDTHSKRTL----L
                                 QGPFDMDSCLSRHSINPYSNRESRIL----FSTWNLDHI-----
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                                                                                                                                                                                                               AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
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Pred. No. 0.62
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COIL 2.
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OCCORDINATION OCCUPANT

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VIME_HUMAN

ID VIME_HUMAN STANDARD;
ID VIME_HUMAN STANDARD;
AC P08670; Q15867; Q9NTM3; Q15869; Q15868;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-CCT-193 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
                                               TISSUE-Osteosarcoma;

MEDLINE-90215314; pubmed-2323579;

Gupta A.K., Aubin J.E., Waye M.M.Y.;

"Isolation of a human vinentin cDNA with a long 3'-noncoding region from a human osteosarcoma cell line (MG-63).";

Gene 86:303-304(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Breast carcinoma;
MEDLINE-89303836; PubMed-2472876;
MEDLINE-89303836; PubMed-2472876;
Sommers C.L., Walker-Jones D., Heckford S.E., Worland P.,
Valverius E., Clark R., McCormick F., Stampfer M., Abularach S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrari S., Battini R., Kaczmarek L., Rittling S., Calabretta B., de Riel J.K., Philiponis V., Wei J.-F., Baserga R.; "Coding sequence and growth regulation of the human vimentin gene."; Mol. Cell. Biol. 6:3614-3620(1986).
                                                                                                                                                                                                                                                                                   Gene 62:7-16(1988).
                                                                                                                                                                                                                                                                                                        Perreau J., Lilienbaum A., Vasseur M., Paulin D.;
"Nucleotide sequence of the human vimentin gene and regulation of its transcription in tissues and cultured cells.";
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=F1broblast;
MEDLINE=88226018; PubMed=3371665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Vimentin rather than keratin expression in some hormone-independent breast cancer cell lines and in oncogene-transformed mammary
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SEQUENCE OF 16-24 AND 54-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 112-465 FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-134 FROM N.A., AND TISSUE SPECIFICITY.
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MEDLINE-97295304; PubMed
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Aarhus/Ghent-2DPAGE; 8417; I
PHCI-2DPAGE; P08670; -
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PIR; S13115; S13115
SWISS-2DPAGE; P0867
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SUBUNIT: HOMOPOLYMER.
TISSUE SPECIFICITY: Highly expressed in fibroblasts, some expression in T and B lymphocytes, and little or no expression is Burkitt's lymphoma cell lines. Expressed in many hormone-independent mammary carcinoma cell lines.
Independent mammary carcinoma cell lines.
FIM: ONE OF THE MOST PROMINENT PHOSPHOPOTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL
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L; X5614; CAA79600.1; ALT_SEO.

L; Z19534; CAA79613.1; CAB97963.1; CAB97963.1; CAB97963.1; CAB97963.1; CAB97963.1; CAB97963.2; CAB34499.1; CAB344499.1; CAB344
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Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
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                                            the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria;
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                                                                                                                                         PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
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Best Local S
Matches 64
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15-JUL-1999 (Rel. 38, C
15-JUL-1999 (Rel. 38, I
15-JUN-2002 (Rel. 41, I
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DOMAIN
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                 Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w code for large proteins in vitro."; DNA Res. 4:141-150(1997).
  -I-
                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                            transforming sequence-like MCF2L OR KIAA0362.
                                                                                                                                                                                                                                                                                                                             15-JUN-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Guanine nucleotide exchange factor DBS (DBL's
transforming sequence-like protein) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DBS_HUMAN
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                                                                                                                                           MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                            NCBI_TaxID~9606;
                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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TE; PS00226; IF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ
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                                                                                                                                                                                                                                                  Eutheria;
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Pred. No.
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LINKER 1.
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                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119E126778BF5801 CRC64;
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  EXCHANGE
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FACTOR THAT POTENTIALLY
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which can
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Best Local S
Matches 83
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Pfam; PF00435; Spectrin; 1.
Pfam; PF00621; RhOGEF; 1.
SMART; SM00233; PH; 1.
SMART; SM00325; RhOGEF; 1.
SMART; SM00315; SR014; 1.
SMART; SM00150; SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKS PATHWAYS THAT SIGNAL THROUGH RAC1, RHOA AND CDC42 CATALYZES GUANINE NUCLEOTIDE EXCHANGE ON RHOA AND CDC42 AND INTERACTS SPECIFICALLY WITH THE GTP-BOUND FORM OF RAC1, SUGGESTING THAT IT FUNCTIONS AS AN EFFECTOR OF RAC1. MAY ALSO PARTICIPATE IN AXONAL TRANSPORT IN THE BRAIN. BECOMES ACTIVATED AND HIGHLY TUMORIGENIC BY TRUNCATION OF THE N-TERMINUS (BY SIMILARITY).

1- SIMILARITY: CONTAINS 1 DEL-HOMOLOGY (DH) DOMAIN.

1- SIMILARITY: CONTAINS 1 CRAL-TRIO DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB002360; BAA20817.1; -. Genew; HGNC:14576; MCF2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00741; DH_1; 1:
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
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                                                                                                                                                                                         153
                                                                                                                                                                                                                      505 DGAEAALQEIEKFLETGAENKIQELNAIYKEYESILNQDLMEHVRKVFQKQASMEEVFHR 564
                                                                                                                                                                                                                                                                                                                                          445 RPKCQELRHLCDQFSAEIARRRGLLSKSLELHRRLETSMKWCDEGIYLLASQPVDKCQSQ 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ne-nucleotide releasing factor; Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                95 PQVGL--IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSK 152
                                                                                                                                                                                                                                                                                                            51 DGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL-----SAFHE 94
                                                                                                                                                                                                                                                                                                                                                                        4 KPKSVKLRAL------RSPRKFGVAGRSCQ-----EVLRKGCLR--FQLPERGSRLCLYE 50
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                   ---KKRTIIPTLV-----EAIKEQDGREVDWEYFYGLLFTSENLKLVHIV 305
                                     RELENYTDCPELVGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE------
                                                                                               ----ELLCVLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
                                                                                                                                                           GGALRRGPYRRAKSEMSESRQGRGSAGEE--EESLAILRRHVMSELLDTER---AYVE--
                                                                                                                                                                                      SGYLRYSCESRIRSYLREVSSYPSTYGAEAQEEFLRYLGS--MCQRLRSMQYNGSYFDRG 210
        CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK 336
                                                                                                                           AKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILESTWNLDHIIE-----
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IPRO01331; GDS_CDC24.
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641
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                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 3
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POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1108;
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                                                                                                                                                                                           POL_SIVMK STANDARD; PRT; 1054 AA.

POS897;
O1-NOV-1988 (Rel. 09, Created)
O1-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.-)
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.
SEQUENCE FROM N.A.

MEDLINE-87287229; PubMed=3497350;

Franchini G., Gallo R.C., Guo H.-G., Gurgo C., Callatti E.,

Fargnoli K., Hall L., Wong-Staal F., Reitz M.S. Jr.;

**Requence of simian immunodeficiency virus and its relations
the human immunodeficiency viruses.";

Nature 328:539-543(1987).

**I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'--
                                                                                                                                        Simian immunodeficiency virus (K6W isolate) (SIV-MAC).
Viruses; Rettroid viruses; Retroviridae; Lentivirus.
NCBL_TaxlD=11735;
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relationship

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RESULT 12
                                                                                      Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96AQ7:
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
:: SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                                                                                                                                   EMBL; BC016851; AAH16851.1; -. InterPro; IPR003508; CAD. Pfam; PF02017; CIDE-N; 1.
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fat-specific protein FSP27 homolog.
FSP27.
                                                                                                                                                                                                                                                                                                                                                                                                    the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        765 CORKLDHKLSLD-SYLLKPVORITKYQLLLK 794
37 PKAPRARPCRVSTADRSVRK-GIMAYSLEDLLLKVRDTLMLADKPFFLVLEEDGTTVETE 95
                                       5 PKSVKLR-----ALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TE 57
                                                                                        33;
                                                                                                             Similarity
                                                                                                                                                                            238 AA;
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics Institute.
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                                                                                                     5.2%;
7 33.3%;
                                                                                                                                                                         118 C
26754 MW;
                                                                                      16; Mismatches
                                                                                Score 92.5; DB 1; Length 238; Pred. No. 0.78; 6; Mismatches 41; Indels
                                                                                                                                                               CIDE-N.
; 5CF774929E821DA5 CRC64;
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BAC2_HUMAN S
ID BAC2_HUMAN S
AC Q9BYV9; Q9NTS5;
DT 15-JUN-2002 (Re)
                                                                                RESULT
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Matches
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HIV; M15897; POLS
MEROPS; A02.002;
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PROSITE; PS00175; ASP_PROT_RETROV; 1.

AIDS; Polyprotein; Hydrolase; Aspartyl protease;

Nuclease; Transferase; RNA-directed DNA polymorn.

CHAIN
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InterPro; IPR000477; RV
InterPro; IPR001584; Rv
Pfam; PF00075; rnaseH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001995; Aspprotease_rtrv.
InterPro; IPR001969; Aspprotease_site.
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InterPro; IPR003308;
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate =
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PF00078;
PF00552;
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PF02022; Integra
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                                                                                                                                                                                                                                                                                                                                                                                 YIYKVLPQGWKGSPAIFQYTMRHVLEPFRKANPDVTLVQYMDDILIASDRTDLEHDRVVL
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    (Rel. 41,
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THE PROTEASE BELONGS
TAMILY.
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Integrase_Zn.
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                                                                                                                                                                                                                                                             -SRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNG
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
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Query Match
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as lon modified and this statement is not remove entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                     Nuclear protein;
DOMAIN 37
                                                                                                                                                                                                                        Pfam; PF00170; bZIP; Pfam; PF00651; BTB;
                                                                                                                                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
Melo J.V., Vieira S.D., Deininger M.W.N.;
"BACH2 expression in leukaemic cells.";
Submitted (FEB-2000) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of human BACH2 mapped to chromosome 6q15." Oncogene 19:3739-3749(2000).
                                                                     DNA_BIND
                                                                                      DOMAIN
                                                                                                                                        Transcription
                                                                                                                                                      PROSITE; PS50097; BTB; 1.
PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                          InterPro; IPR000210; InterPro; IPR004827;
                                                                                                                                                                                                                                                                                             MIM; 605394;
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Muto A., Nagai H., Kinoshita T., Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-20404861; PubMed-10949928;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                produced by alternative splicing.
TISSUE SPECIFICITY: B-cell specific.
SIMILARITY: BELONGS TO THE BZIP FAMILY. CNC
SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitted (APR-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REPRESSOR OF ACTIVATOR. BINDS TO MAF RECOGNITION ELEMENTS (MARE). PLAY IMPORTANT ROLES IN COORDINATING TRANSCRIPTION ACTIVATION AND REPRESSION BY MAFK (By similarity).
SUBUNIT: Heterodimer of BACH2 and Maf-related transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Heterodimer of lactors (By similarity).
                                                                                                                                                                                                                                                                                                                                                                               AF357835;
AJ271878;
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SM00225; BTB; 1.
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651
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416
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etazoa; Chordata; Craniata; Vertebrata;
+heria: Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Igarashi K., Yokoyama M.;
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                                                                                                                                        regulation;
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                                                                   POLY-GLU.
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to M., Inazawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        % A.F..
Gallus gallus (Chicken),
Gallus gallus (Chicken),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                   MEDITINE-813195052; PubMed-6573660;

Zehner Z.E., Paterson B.M.;

Zehner Z.E., Paterson B.M.;

"Characterization of the chicken vimentin gene: single copy gene producing multiple manas.";

Proc. Natl. Acad. Sci. U.S.A. 80:911-915(1983).

-I- FUNCTION: Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells.

-I- SUBUNIT: HOMOPOLYMER.

-I- PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS OF MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIME_CHICK STANDARD; FALL CONTROL OF CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zehner Z.E., Li Y., Roe B.A., Paterson B.M., Sax "The Chicken vimentin gene. Nucleotide sequence, and comparison to the hamster gene"; J. Biol. Chem. 262:8112-8120(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87250401; PubMed=3036797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE OF 453-459 FROM N.A.
                       SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                            REORGANIZED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 YKPQTRLK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 REVSSYPSTVGA-----EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 VDWEYFYGLLFTSENLKLVHIV-------CHKK-----TTHKLNCDPSRI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 FSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGRE
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Mismatches 136; Indels 161;
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RESULT 16
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Best Local &
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POL_SIVSP STANDARD; PRT; 1022 AA.
P19505; Q88140;
01-FEB-1991 (Rel. 17, Created)
101-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin)
Reverse transcriptase (EC 2.7.7.49); Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M15852; AAA49134.1;
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                                                                                                                                                                                                                                                                                  441 ETRDGQVIN 449
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M15851; AAA49134.1;
V00447; CAA23726.2;
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ilament; Coiled coil; Phosphorylation.
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COIL 1A.
LINKER 1.
COIL 1B.
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Pred. No.
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LINKER 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 459;
              (EC 3.4.23.-);
H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SCESRIR----SY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------DLLNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
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POL.

Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11738;

Simian immunodeficiency virus (PBj14/BCL-3 isolate) (sooty mangabey)

SEQUENCE FROM N.A. MEDLINE=90272009; PubMed=1971917;

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Matches 56
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InterPro; IPR001969; /
InterPro; IPR001037; InterPro; IPR003308;
                                                                                                                                                                                                                                                                           Pfam; PF02022; Integrase_Zn; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
AIDS; POlyprotein; Hydrolase; Aspartyl protease; Er
Nuclease; Transferase; RNA-directed DNA polymerase.
CHAIN
CHAIN
1 1 70
PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS Res. Hum. Retroviru-
-1- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dewhurst S., Embretson J.E., "Sequence analysis and acute SIVSMM-PBj14.";
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dewhurst S., Embretson J.E., Fultz P.N., Mullins J.I.; "Molecular clones from a non-acutely pathogenic derivative SIVsmmPBJ14: characterization and comparison to acutely pathogeness."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. meDLINE-92368737; PubMed-1503826;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; A02.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: CLEAVAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. There by non-profit institutions as long as ifled and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: THE PROTEASE BELONGS KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphomonoester.
CATALYTIC ACTIVITY: N deoxynucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DETERMINED.
SIMILARITY:
                              377
                                                        121
                                                                                                                                                                                                                                                                                                                                                    PF00552;
PF00665;
PF02022;
  159
                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                           PF00075; rnaseH; 1.
PF00077; rvp; 1.
PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M31325; AAA47753.1;
L03298; AAA47777.1;
                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DNA) (N)
                                                                                                                                                                                                              Similarity
SCE-
                                                       DLLHNVSQNIAAETRAEDPPW-FEGLE
                          ELLNSIGFSTPEEKFQKDPPFQWMGYELWPTKWKLQKIELPQRETWTVNDIQKLVGVLNW
                                                                                 KVLPQGWKGSPAIFQHTMRNVLEPFRKANPDVTLIQYMDDILIASDRTDLEHDRVVLQLK 376
                                                                                                                LTLGQAWQG----
                                                                                                                                                                    PRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAE----LVL 71
                                                                                                                                        PHPAGLAKRRRITVLDVGDAYFSIP--;----LDEEFRQYTAFTLPSV-NNAEPGKRYIY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002156;
                                                                                                                                                                                                                                                       96
1022
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POL$SMMPBJ.
                                                                                                                                                                                                                                                                                                                                                                              integrase; 1.
                                                                                                                                                                                                                                                                                                                                                                    rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retroviruses 8:1179-1187(1992).
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                                                                                                                                                                                                          5.1%;
23.0%;
                                                                                                                                                                                                                                                    96 BY SIMILARITY
115869 MW; 16DFBEA03
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Aspprotease_site.
Integrase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integrase_Zn.
                                                                                                           -YVSDIRRFLSAFHE--PQVGLIQAAQQLL--CDEQAPQRQRL---LA 120
-SRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endonucleolytic
                                                                                                                                                                                                32;
                                                                                                                                                                                                           Score 90.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIELD THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson D.C., Mullins J.I., Fultz P.N., pathogenicity of molecularly cloned
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                     16DFBEA03F289D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cleavage
                                                                                                                                                                                                           6,
                                                                                                                                                                                                                           멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triphosphate -
                                                                                                                                                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and the
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                                                                                                                                                                                                                                                                                                           Endonuclease;
                                                                                                                                                                                                                          Length 1022;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REMAIN TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Α2;
                                                       SRFQSKSGYLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N diphosphate
                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration -
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Q64096;
                                                                  SMART; SM
SMART; SM
SMART; SM
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitehead I., Kirk H., Kay R.; "Retroviral transduction and oncogenic selection of a Dbs, a homolog of the Dbl guanine nucleotide exchange Oncogene 10:713-721(1995).
                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:103263; MCf21.
InterPro; IPR001251; CH
InterPro; IPR001331; GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hematopoietic;
MEDLINE=95166559; PubMed=7862449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCF2L OR DBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guanine nucleotide exchange factor DBS (DBL's
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yeane 10:713-721(1995).

ogene 10:713-721(1995).

FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACT.

LINKS PATHRAYS THAT SIGNAL THROUGH RAC1, RHOA AND CDC42.

GUANINE NUCLEOTIDE EXCHANGE ON RHOA AND CDC42 AND INTERACTS

SPECIFICALLY WITH THE GIP-BOUND FORM OF RAC1, SUGGESTING THAT IT

FUNCTIONS AS AN EFFECTOR OF RAC1. MAY ALSO PARTICIPATE IN AXONAL

TRANSPORT IN THE BRAIN. BECOMES ACTIVATED AND HIGHLY TUMORIGENIC

BY TRUNCATION OF THE N-TERMINUS (BY SIMILARITY).

BY TRUNCATION OF THE N-TERMINUS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by an
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SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH)
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 CRAL-TRIO DOMAIN.
                                                                                                                                        ; PF00621; RhoGEE
T; SM00233; PH; 1
T; SM00325; RhoGE
T; SM00516; SEC14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
                                                                                                                                                                                                          PF00435; spectrin; 1.
PF00621; RhoGEF; 1.
                                                                                           SM00326;
SM00150;
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                   PS50191; CRAL_TRIO; PS00741; DH_1; 1. PS50010; DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OEG
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                                                                                                                                                                                                                                                                                                                                                          IPR001849;
IPR000219;
                                                                                                                                          16; SEC14;
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                                                                                         SH3; 1.
SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                      GDS_CDC24
                                                                                                                                                                                                                                                                                                                                                                                                                                    CRAL_TRIO
                                                                                                                                                                                                                                                                                                           Spectrin
                                                                                                                                                                                                                                                                                                                                                          RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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factor.";
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

8 Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

8 Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

8 Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

8 Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

8 Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

8 Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

8 Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

9 Oliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,

8 Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

8 Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,

8 Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

8 A Taylor K., Taylor R.G., Tivey A., Walsh S., V., Warren T., Whitehead S.,

8 Woodward J., Volckaert G., Aert R., Robben J., Germonprez B.,

8 A Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

8 Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

8 A Eger P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATC6_SCHPO STANDARD; PRT; 1211 AA.
014072; Q9UT01; Q9USD0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cation-transporting APPase C2E11.07C
SPACZEI1.07C OR SPACUNK4.07C OR SPAPYUK71.01.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).

Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guanine-nucleotide
DOMAIN 52
DOMAIN 624
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21848401; PubMed-11859360;
Wood V., Gwilliam R., Rajandream א
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 LDTERAYVEELLCVLEGYAA-----EMDNPLMAHLISTGLQNKKNILFG--NMEEIYHFH 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 CLYEDGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRNIPAGVESCIDCPELVGRCFLERMEEFQIYEKYCQNKPRSESLWRQCSDCPFFQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTIIPTLVEA---IKEQDGR----------EVDWEYFYGLLFTSENLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENSSSEGNALRRGPYRRAKSEMSEPRQGRTSSTGEE--EESLAI-----LRRHVMNEL 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRFQSKSGYLRYSCESRIRSYLREV-SSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VF-----QKQESTEEMFHRRQASLKKLAAKQTRPVQPVAPRPEALTKSPSPSPGSWRSS 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLCDEQAPQRQRLLADLLH----NVSQNIAAETRAEDP--PWFEGL-----E 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQSQDGAEASFQEIEKFLETGAENKIQELNEIYKEYECILNQ------DLLEHVQK 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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22.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 90.5; D
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3.
WW; D9100DD133BEA9E3 CRC64;
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CRAL-TRIO.
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EMBL; AL031180; CAA20137.1; -.
EMBL; AL109734; CAB52144.1; -.
EMBL; AB027853; BAA87157.1; -.
EMBL; AB027853; BAA87157.1; -.
InterPro; IPR001757; AfPase_E1-E2.
InterPro; IPR001454; Hignase/hydrlase.
Pfam; PF00122; E1-E2_AfPase; 1.
PfAm; PF00123; E1-E2_AfPase; 1.
PRANTS; PR00119; CATAPPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G. Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
wature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fission yeast cells by the use of a GFP-fusion genomic Genes Cells 5:169-190(2000).

Genes Cells 5:169-190(2000).

-I- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

-I- SUBCELLOUAR LOCATION: Integral membrane protein.

-I- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ding D.Q., Tomita
Hiraoka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=968 h90;
MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 617-809 FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale screening of intracellular protein localization in living ission yeast cells by the use of a GFP-fusion genomic DNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPASES). SUBFAMILY V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N: Integral membrane protein.
TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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SEQUENCE TRANSMEM TRANSMEM TRANSMEM DOMAIN PROSITE; PS00154; ATPASE_E1_E2; FRANSMEM FRANSMEM RANSMEM RANSMEM RANSMEM RANSMEM RANSMEM lydrolase; RES Transmembrane; 996 1016 1023 1040 1058 1082 1102 11125 11136 11156 11173 11196 ₽¥, 452 995 1015 1022 1022 1039 1057 1081 136260 Phosphorylation; Magnesium; ATP-binding.
CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY). EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL) MAGNESIUM CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL). POTENTIAL EXTRACELLULAR (POTENTIAL). POTENTIAL CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL) POTENTIAL 6FEE4228CA5A57EC CRC64; ASMIC (POTENTIAL). ELLULAR (POTENTIAL).

Query Match Best Local

Similarity

5.0%; 20.7%;

Score 90; Pred. No.

DB 1; 10;

Length 1211;

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GAPE_RABIT
ID GGERE_R
AC P56201
DT 01-NOV
DT 30-NOV
DT 30-NOV
DT 30-NOV
DT GDH
DE GHOYGE
DE GHOYGE
DE HOOSPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p56201;
01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GDH/6PGL endoplasmic bifunctional protein [Includes:
dehydrogenase (EC 1.1.1.47) (Hexose-6-phosphate dehyd
dehydrogenase (EC 3.1.1.31) (6PGL)].
                                                                                                                                                                                                                                                   lactone + NAD(P)H.
-i- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NAD(P)(+) =
1,5-lactone 6-phosphate + NAD(P)H.
-i- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(
                                                                                                                                                                                                                                                                                                                                                 "Isolation and the complete amino acid sequence of lumenal endoplasmic reticulum glucose-6-phosphate dehydrogenase."; Proc. Natl. Acad. Sci. U.S.A. 90:5302-5306(1993).
-1- FUNCTION: OXIDIZES GLUCOSE-6-PHOSPHATE AND GLUCOSE, AS
                                InterPro; IPR000457;
Pfam; PF00479; G6PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                               InterPro; IPR001282; G6PD.
InterPro; IPR000457; Glucosamine_iso.
                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: Beta-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93281746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G6PE_RABIT
                                                                                                                                       SUBCELLULAR LOCATION: MICROSOMES, ENDOF
SIMILARITY: IN THE N-TERMINAL SECTION;
PHOSPHATE DEHYDROGENASE FAMILY:
SIMILARITY: IN THE C-TERMINAL SECTION;
GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE I
                                                                              PHOSPHOGLUCONOLACTONASE SUBFAMILY.
CAUTION: THE SEQUENCE IN REF.I SEEMS
TRANSPOSITION OF A SECTION THAT WAS P
WHICH IS NOW TRANSPOSED TO POSITION 5
                                                                                                                                                                                                      Phospho-D-gluconate.

Phospho-D-gluconate.

COFACTOR: CAN USE BOTH NAD OR NADP.

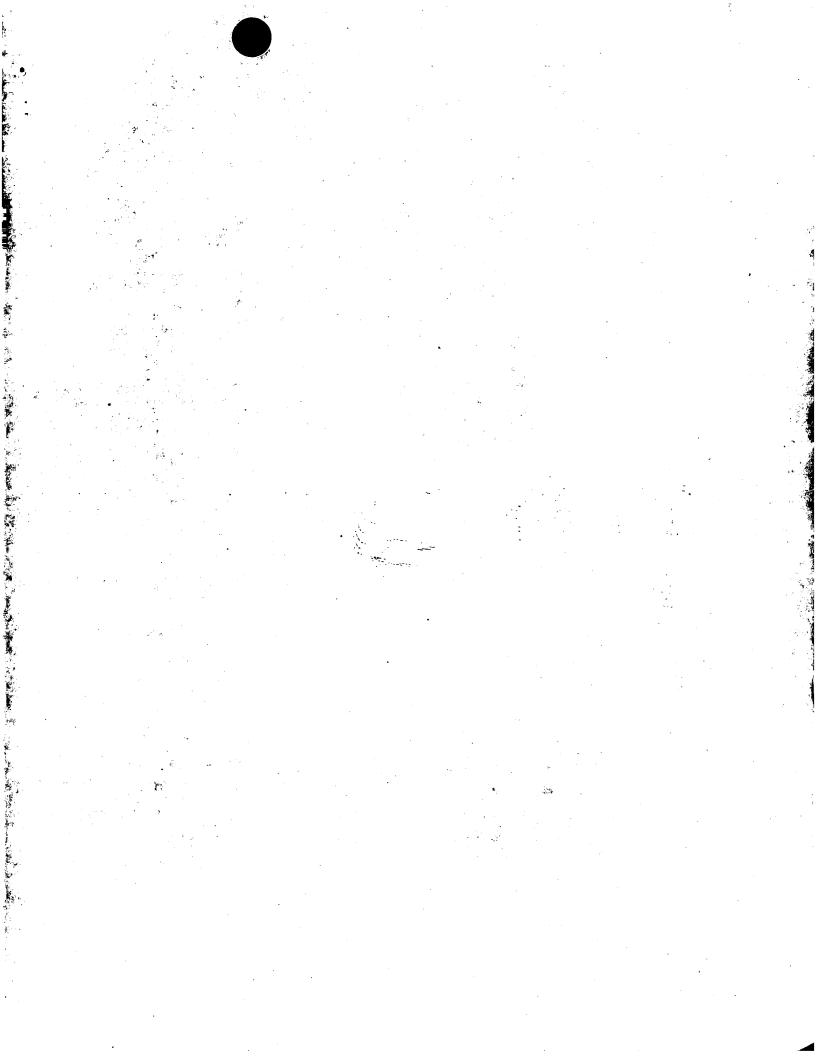
COFACTOR: TOTAL MICROSOMES, ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                       OTHER HEXOSE-6-PHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Zealand white; TISSUE-Liver;
281746; PubMed-8506377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cuniculus (Rabbit).
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Glucosamine_iso;
G6PD_C; 1.
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Lagomorpha;
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; Leporidae; Oryctola;
                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
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                                                                                POSITION 700.
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dehydrogenase);
                                                                                                                                                                                          RETICULUM LUMEN.
S TO THE GLUCOSE-6-
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                                                                                              ö
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       Development 105:299-307(1989).

-I - FUNCTION: DESMIN ARE CLASS-III INTERNEDIATE FILA MUSCLE CELLS. IN ADULT STRIATED MUSCLE THEY FORM NETWORK CONNECTING MYOFIBRILS TO EACH OTHER AND MEMBRANE FROM THE PERIPHERY OF THE Z-LINE STRUCT
                                                                  SEQUENCE FKUM N.A.
MEDLINE=90032404; PubMed=2806128;
Herrmann H., Fouquet B., Franke W.W.;
"Expression of intermediate filament proteins dur
                                                                                                                                               Eukaryota; Metazoa; Chordat; Amphibia; Batrachia; Anura; Xenopodinae; Xenopus.
                                                                                                                                                                                         DES
                                                                                                                                                                                                                       01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00069; G6P_DEHYDROGENASE; 1. Oxidoreductase; NAD; NADP; Glucose metabolism;
                                                              desmin."
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                             Xenopus laevis
                                                                                                                                                                                                   Desmin.
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Chordata; Craniata; Ve
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Last sequence update)
Last annotation updat
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PYRROLIDONE CARBOXYLIC
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Pred. No. 6.3;
47; Mismatches
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                  THE PLASMA
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Best Local Similarity
Matches 49; Conserv
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SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A43554; A43554.
InterPro; IPRO01664; IF.
Pfam; pP00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Muscle protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X16842; CAA34740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic.
357 -RLEEEIRNMKDEMARHLREYQ 377
                            180 AEAQEEFLRVLGSMCQRLRSMQ 201
                                                               301 AMRQSKQEMMEYRHQIQS----YTCEIDALKGTNDSLMRQMRDLEEKFSGEAAGYQDTIG 356
                                                                                                                                                                                             183 QEEIQLKEDAENNLAAFRGDYDAATLARIDLERRIESLQEEI-AFLKKIHEEEIRELQAQ 241
                                                                                             143 ------SYLREVSSYPSTVG 179
                                                                                                                                                               242 FQEQQLQVEIDVSKPDLTAALRDIRAQY-ENIAAKNVAEAEEWYKSKVSDLNQAAKKNND 300
                                                                                                                                                                                                                            50 EDGTELTED-----YFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQA- 102
                                                                                                                                                                                                                                                                                                                                 458 AA;
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                               52802 MW;
                                                                                                                                                                                                                                                                              4.9%; Score 88.5; DB 1; Length 458; 24.3%; Pred. No. 4;
                                                                                                                                                                                                                                                              24; Mismatches
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2B.
COIL 2B.
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                                                                                                                                                                                                                                                            72; Indels
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Search completed: May 26, 2003, 15:21:38 Job time: 23 secs



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Result
No.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a \mathcal{Q} score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                              Score
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1789
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/SIDS2/gcgdata/geneseq/geneseqp-embl
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               Caspase activated Mouse caspase acti
Mouse caspase acti
Human polypeptide
Drosophila melanog
Human vimentin. H
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Amino acid sequenc
Human DNA fragment
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Human prostate			366	4.9	87	45	
			331	4.9	87	44	
Human DFF45 prote			331	4.9	87	43	
Pol gene product			1035	4.9		42	
יסי			646	4.9	7.	41	
Mouse huntingtin-		21	756	4.9	88	40	
Novel human diagno	ABG0816	22	613	4.9	88	39	
Deduced sequence	×	9	3210	4.9		38	
Sequence of clone		1	3080	4.9	88.5	37	
Human vimentin.	3 ABB77394	2	465	4.9	8	36	
Protein #4 related		23	429		88.5	35	
		N	331		89	34	
_	AAG6359	22	331	٠	68	33	
_		2	331	5.0	89	32	
		N	160	٠	89	31	
		ນ	142	5.0	89	30	
Human breast tumou		2	135		89	29	
		22	5322	5.0	89.5	28	
phila me		2	1719		91	27	
CIDE-		2	219		91	26	
Amino acid sequenc		2	907		ŗ	25	
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human		23	214			20	
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protein	_	22	1120		93.5	17	
-		N	1152		٠	16	
Human pancreatic		23	466		97	15	
Human vimentin.		22	466	5.4	97	14	
11		21	466	5.4	97	13	
4	AAW54	19	465	5.4	97	12	
Mouse ischaemic	3 ABB57310		466	5. 5	99	ï	

ALIGNMENTS

RESULT 1

ANY57440

ID AAY57440;

XX

AC AAY57440;

XX

AC AAY57440;

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AC AAY57440;

XX

DT 22-FEB-2000 (first entry)

XX

DE Human DNA fragmentation factor DFF40 protein sequence.

XX

KW Human; DNA fragmentation factor; DFF40; DFF45; apoptosis; gene therapy;

XX

Cytostatic; growth; tumour.

XX

BOS Homo sapiens.

XX

W09954482-A1.

XX

PD 28-OCT-1999.

XX

PD 28-OCT-1999.

XX

PR 16-APR-1998; 98WO-US07895.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

DNA fragmentation factor DFF40 involved in apoptosis and related polynucleotide

WPI; 2000-052702/04. N-PSDB; AAZ38992. Wang X,

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                                                                 02-AUG-2001
                                                                                                US2001011078-A1
                                                                                                                                                              molecular chaperone;
                                22-DEC-2000;
                                                                                                                                Homo sapiens
                                                                                                                                                                                 Human;
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592
AAG63592 standard;
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 6-APR-1998;
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                                                                                                                                                                             fragmentation factor; DFF40; DFF45; apoptosis; DNase
                                                                                                                                                                                                             sequence
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ilarity 100.0%;
Conservative
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CBE1-900-SIIB6
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                                                                                                                                                                                                               of human
                                                                                                                                                              cancer cell
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Pred. No. 8.8e-167;
Mismatches 0;
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                                                                                                         Human DNA fragmentation factor 40 (DFF40).
                                                                 Human; DNA fragmentation factor;
gene therapy; hyperproliferative
psoriasis; angiogenesis; cancer;
                                                                                                                                                               AAY72467;
                                                                                                                                                                                       AAY72467 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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nilarity 100.0%;
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Pred. No. 8.
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                                                                 DFF; apoptosis; molecular chaperone;
disorder; therapy; tumour; restenosis;
cytostatic; neoplasia.
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d.8e-167;
es 0;
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26-DEC-2000 US6165737-A. Homo

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying modulator of human DNA fragmentation factor 40, for treating cancer, involves contacting cell or cell-free composition comprising DFF40 with candidate substance and comparing apoptosis with control
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N-PSDB; AAD02498.
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  Caspase activated nuclease CPAN
                                        11-JUN-1999
                                                                                 AAY04123;
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llarity 100.0%;
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Pred. No. 8.8e-167;
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Best Local :
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22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caspase activated nuclease; CPAN; apoptosis; human; heart attack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated caspase activated nuclease - used to develop products which can inhibit or activate apoptosis for use in treating e.g. heart attack, stroke or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9910501-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stroke; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 38; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX19907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-190620/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      active.
                                                                                                                                                                                                            121 DLLHNVSQNIAAETRAEDPFWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180
                                                                                                                                                        181
                                                                                                                                                                                      121
 301
                   301 LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                             241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300
                                                                                                                       181 EAGEEFLRVLGSMCQKLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                             241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                                                                                                                                                                                                                        al Similarity 99. 337; Conservative
                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                          EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGFFDMDSCLSRHS
                                                                                                                                                                                                                                                                  PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120
LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                                                     DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA
                                                                                                                                                                                                                                                  PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MacDonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0072192.
97US-0056904.
97US-0056907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US17214.
                                                                                                                                                                                                                                                                                                                                                                                      99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ή
                                                                                                                                                                                                                                                                                                                                                                      Score 1786; DB 20;
Pred. No. 1.7e-166;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 338;
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                             300
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 RESULT 6
AAY29936
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Best Local S
Matches 261
                                                                                                                                                                                                                                                                                                                                                              The present invention describes an inhibitor (ICAD) for caspase-activating DNase (CAD). Two ICAD's are specifically claimed: a long chain form (ICAD-L) and a short chain form (ICAD-S). ICAD and ICAD CDNA can be used in the prevention of cell death, and can be used as a research reagent for cell death. The present sequence represents mouse CAD which is used in the exemplification of the present invention.
          AAY29936 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibitor for caspase-activating DNase - useful for preventing death and is useful as reagent for cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-554024/47.
N-PSDB; AAZ21173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; caspase cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP11239495-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse caspase-activating DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY29931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY29931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO
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                                                             302
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                          DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180
                                                                        LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                    EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                                                                                                      | CHAPPECVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCF
                                                                                                                                                                                                                                                                                MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                            INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                                DLLHHVSQNITAETREQDPSWFEGLESRFRNKSGYLRYSCESRIRGYLREVSAYTSMVDE
                                                                                                                                                                                                                                  PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
                                                           LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR
                                                                                                 INPYGNRESRILFSTWNLDHIIEKKRTVVPTLAEAI--QDGREVNWEYFYSLLFTAENLK
                                                                                                                                         AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
                                                                                                                                                                                                                                                                                                   79.2%;
illarity 77.2%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                             344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     16-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-0369356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activating DNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0369222
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                                                                                                                                                                                                                                                                                                                                                                                                                                    26pp; Japanese.
                                                                                                                                                                                                                                                                                                     Score 1416; DI
Pred. No. 3.6e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAD;
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                                                                                                                                                                                                                                                                                                              DB 20;
                                                           339
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                        Length 344;
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RESULT 7
AAO09550
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Matches 261;
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                                                                                      AAO09550 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents mouse caspase activating DNase (CAD). CAD can be used for the removal of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 14-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; caspase activating DNase; CAD; cell death; cancer. '
Human polypeptide
                              06-NOV-2001
                                                            AA009550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New caspase-activating DNase - useful for eliminating cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-554023/47.
N-PSDB; AAZ21180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse caspase activating DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP11239494-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO
                                                                                                                                                                  302
                                                                                                                                                                                            301
                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                 184 AAQEEYLRVLGSMCQKLKSVQYNGSYFDRGAEASSRLCTPEGWFSCQGPFDLESCLSKHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                LVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ
                                                                                                                                                                                                                                       INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK
                                                                                                                                                                                                                                                                                                                                                                                               LVHIACHKKTTHKLECDRSRIYRPQTGSRRKQPARKKR
                                                                                                                                                                                                                        INPYGNRESRILFSTWNLDHIIEKKRTVVPTLAEAI--QDGREVNWEYFYSLLFTAENLK
                                                                                                                                                                                                                                                                                                              EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA;
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                              (first
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 SEQ ID NO 23442.
                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.2%;
77.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1416; DB 20;
Pred. No. 3.6e-130;
7; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor; ICAD;
                                                                                                                                                                339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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cell proliferation;

cell differentiation;

gene

therapy;

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ARESULT 8
ARB64476
ID ARB66
AC ARB66
AC ARB66
AC ARB66
XX 26-M
XX 26-M
XX DTOS
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est Local S
tches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proteins or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.
                                                                     Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 23442; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundisorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                       Drosophila melanogaster
                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 20010.
                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                 ABB64406;
                                                                                                                                                                                                                                                                               ABB64406 standard; Protein; 450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                   294 FTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 SCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLL 293
                                                                                                                                                                                                                                                                                                                                                                                            52 FTSENLNLVHIVCHKKTTHKLTCDSSSIYYPQTRLKRKQPVRKRQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LMSRWG--YRIEKKRTIIRSVVEAIKEQDGREVDWEYFYGLL 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 372; DB 22;
Pred. No. 1.4e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 9
AAY92335
ID AAY9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental blology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                     AAY92335 standard; Protein; 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a,t ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20010; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes from Drosophila
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2001.
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                                                                                                                                       400
                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 P--DAVITTDADFEFEKMRQQSPLLKVA-DIFYDFIEQHPEKFRRMITEYEHQKQRRVLD 171
                                                                                                                                                                               294 FTSENLKLVHIVCHKK-----TTHKLNCDPSRIYK 323
                                                                                                                                                                                                                                                                                                                    281 RIPSKRLRQVIREYTKENCILDEWSTSLCSDLGDFYCQGSYSENGNSCSKQHTINPYASR 340
                                                                                                                                                                                                                                                                                                                                                                                                           221 TRNPLYRQNAKARQVINSVLEKFRYLLIGCDFFSMMFDRNCKQKHEFLKQHLGDEETDAG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 NSKTHLSLKAEHVEWFTGGEERFHSKEEAMATRAQTRVRGYY-----YKAKEEL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 RKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTED-YFPSVPDNAELVLLTLG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 QAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD--EQAPQR-QRLLADLLHNVSQNIAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                    FSLKNLKLVHIVCHEKAQRSNRSNGRLLCSDCHEYR 435
                                                                                                                                                                                                                         ENLILFQVWNLDHQIELCRTILPALVANVEELVSHPQTKCSIHKKQVVDISVLEYFLE-I 399
                                                                                                                                                                                                                                                                                                                                                            LR------VLGSMCQRLRSM----QYNGSYFDRGAK------ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ET-----RAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKYGIGANSLEMLIAKAKSKFPLLE--PHLYLASDGFEVSDDEYLKSLP--AQTLFIVSG 114
                                                                                                                                                                                                                                                                         ESRILFSTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD---WEYFYGLL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 321; DB 22;
Pred. No. 1.4e-22;
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Length 450;

invention

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AAY92335

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sequences, etc. are useful for treating or preventing a disease or disorder involving aberrant levels of the complex or protein. Such disorders include cancer, hyperproliferative disorders, neurodegenerative disorders, cardiomyopathies, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New complex of a NLK1 protein and a NLK1 protein-interacting protein, useful for treating cancer, hyperproliferative disorder, neurodegenerative disorder, cardiomyopathies, viral infections and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologue of the Aspergillus nidulans mitotic regulator, NIMA kinase. NIK1 is a serine/threonine-specific kinase and is thought to play a k role in cell-cycle events leading to the onset of mitosis. The complexes, their derivatives and NIK1 or NIK1-IP protein and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interacting proteins. The invention concerns purified complexes of NLK1 protein and a NLK1 protein interacting protein, where the interacting protein is chosen from TrkA, protein phosphatase lalpha, interacting protein is chosen from TrkA, protein phosphatase lalpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY92331-37 were isolated in a modified yeast two hybrid system using NNK1 protein as "bait". These are known sequences which are NNK1 interacting proteins. The invention concerns purified complexes of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA09307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiviral; neuroprotective; cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human vimentin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-3, IP-4, or IP-5. NIK1 (also referred to as Nek2) is a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 145-147; 172pp; English
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       227
                                                                                                                                                                                                                                                                                                                                                                                                                   87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR
                                                                                                                                     YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                               AFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDIMR----LREKLQEE-----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
       QGPFDMDSCLSRHSINPYSNRESRIL--
                                                                    FAVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ---
                                                                                                                                                                                                             YKSKFADLSEAANRNNDALROAKOESTEYRROVOSLTCEVDALKGTNESLEROMREMEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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20.8%;
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                                                                                                                                                                                                                                                                                 -EGLESRFQSKSGYLRY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 21;
Pred. No. 0.9;
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---FST-----WNLDHI----IEKKRTIIPTL 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 466
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                                                                                                                                                                                                                                                                              -SCESRIR----S 166
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                                                                -DLLINV
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RESULT 10
AAB66349
ID AAB66
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                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vimentin;
systemic l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides an antibody which reacts with a cleavage product of vimentin but not with the intact protein. This can be used to detect apoptosis, which may then be used as an indicator of the progression of diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Basedow's disease and acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody reacting with a cleavage product of vimentin but not with
the intact vimentin, useful for detecting apoptosis and the quantity of
cleavage product of vimentin or as a reagent for immunohistochemical
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB66349,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66349 standard; peptide; 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                          142
                                                                                                                                                                                                                                                180 EDIMR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-149349/16
                                        167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                   291
                                                                                                                                                                232 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 VEAIKEQDGREVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTL---L
                                                                                                                                                                                                       87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW
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                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                    Similarity
FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ--
                                                                                                                                                                                                                                                                                      QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR
                                                                               YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caspase cleavage site; apoptosis; antibody; Basedow's
lupus erythematosus; autoimmune haemolytic anaemia; AII
                                                                                                                                                                                                                                                                                                                                                                                                                  466
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 12-14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000EP-0305736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                A,
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                                                                                                                                                                                                                                                                                                                                                    5.5%;
20.1%;
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                                                                                                                          -EGLESRFQSKSGYLRY---
                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                    Score 99; DB
Pred. No. 0.9;
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                                                                                                                                                                                                                                                                                                                                 113;
                                                                                                                                                                                                                                                                                                                                                                        Length 466
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                        SCESRIR----S
                                                                                                                                                                                                                                                                                                                               90;
-DLLNV
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389
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RESULT 11
ABB57310
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                                                                                                                         Query Match
Best Local S
                                                                                                         Matches
                                                                                                                                                                                         The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of gene group comprising these genes. The expression profile or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB57310 standard; Protein; 466
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 2178-2180; 2690pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-034733/04.
N-PSDB; ABI99777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse ischaemic condition related protein sequence SEQ ID NO:867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB57310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 IKTVETRDGQVIN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 VEAIKEODGREVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 KMALDIEIATYRKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---L 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227
                                            180 EDIMR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
                                                                                                       63;
                                                                         27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGPFDMDSCLSRHSINPYSNRESRI-----LFSTWNLDHI-----IEKKRTIIPTL 272
                                                                                                                                                                   466 AA;
                                                                                                     5.5%; Score 99; DB 23; Length 466;
1larity 20.1%; Pred. No. 0.9;
Conservative 47; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii Y;
                                                                                                     90;
                                                                                                       Gaps
                                                                                                       14;
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AAW5435
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      Query Match
Best Local S
Matches 65
                                                                                                                                                                        Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemical markers of human endometrium - useful for, diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-207057/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Byrjalsen I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1997;
06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW54351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW54351 standard; protein; 465 AA
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 20; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLIN-) CENT CLINICAL & BASIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 IKTVETRDGQVIN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 VEAIKEQDGREVD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 KMALDIEIATYRKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---L 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ------
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ch 5.4%; Score 97; DB 19; Length 465; l Similarity 20.8%; Pred. No. 1.4; 65; Conservative 46; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGPFDMDSCLSRHSINPYSNRESRI-----LFSTWNLDHI-----IEKKRTIIPTL 272
                                                                                                                        465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0007132.
96GB-0018600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g.
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179 EDIMR----LREKLQEE----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 230

27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86

90;

Gaps

87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141

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LT 13
9635
AAB29635 standard; Protein;
The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific ISE (Immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis gene 795; to expression constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 795 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids; and a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagasu T, Su
Obayashi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pollinosis-associated gene 795; vimentin homologue; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced detection; diagnosis; drug screening; allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687343/67.
N-PSDB; AAC64226.
                                                                                                                                                                                                                                                                                                               Pollinosis-associated in subjects with high diagnosis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-2000
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                                                                                                                                                                                                                                                                              Page 64-67; Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokoi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2000; 2000WO-JP02734.
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EISAI
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                                                                                                                                                                                                                                                                                                             gene 795 undergoing significantly low expression cedar pollen-specific IgE levels, useful in diseases and screening drug candidates
                                                                                                                                                                                                                                                                              73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kashiwabara T, Oshida T, Obayashi M, Gunji
Yoshida N, Ogawa K, Matsui K, Takahashi E;
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Matches 65
                                                                                                                                                                        Vimentin;
systemic 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative a control. Pollinosis-associated gene 795 is useful in the diagnosis of a lergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a protein encoded by human pollinosis-associated gene 795.
                                                                                                                                                                                                              Human vimentin
 Morishima
                        (RIKE ) RIKEN
                                                 07-JUL-1999;
                                                                          07-JUL-2000; 2000EP-0305736
                                                                                                  10-JAN-2001
                                                                                                                           EP1067142-A1
                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                        caspase cleavage site; apoptosis; antibody; Basedow's dis
lupus erythematosus; autoimmune haemolytic anaemia; AIDS;
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Nakanishi
                                                  99JP-0193235
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 Shibata
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Pred. No. 1.4;
46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides an antibody which reacts with a cleavage product of vimentin but not with the intact protein. This can be used to detect apoptosis, which may then be used as an indicator of the progression of diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Basedow's disease and acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                          07-AUG-2000; 2000US-223130P.
30-JAN-2001; 2001US-265447P.
15-MAY-2001; 2001US-291201P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pancreatic tumour protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU87694;
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                                                                                                                                                                                             Pyle RA, Xu J, Kalos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2001; 2001WO-US24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Novel polynucleotide encoding pancreatic tumour polypeptides, useful in
                                                                               N-PSDB; ABK44209.
                                                                                                                  WPI; 2002-241741/29.
                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
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RESULT 16 AAM79837

AAM79837 standard; Protein; 1152 AA

06-NOV-2001 (first entry)

Human protein SEQ ID NO 3483.

AAM79837;

PD XXX

09-AUG-2001

Homo sapiens. WO200157190-A2 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient. A composition comprising the polynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosis, prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the development of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays.

AAU87689-AAU87694 represent human pancreatic tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of cDNA sequences (ABK44061-ABK4209) encoding human pancreatic tumour proteins. The polynuclectide sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynuclectides is useful for determining the presence of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 165-167; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                         273 VEAIKEQDGREVD 285
                                                                                              390 KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTF---L
                                                                                                                                                                                                                                    167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
                                                                                                                                                                                                                                                                                                                                   142 F-----SCESRIR----S
                                                                                                                                                                                                                                                                                                                                                                                     232 AFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 EDIMR----LREKLQEE-----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
444 IKTVETRDGQVIN 456
                                                                                                                                                                                  351 FAVEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ------
                                                                                                                                                                                                                                                                                    291 YKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEEN: 350
                                                                                                                                                                                                                                                                                                                                                                                                                               87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                     QGPFDMDSCLSRHSINPYSNRESRIL----FST----WNLDHI----IEKKRTIIPTL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%; Score 97; DB.23; Length 46
.20.8%; Pred. No. 1.4;
ative 46; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .23; Length 466;
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809 CQRKLDHKLSLD-SYLLKPVQRITKYQLLLK 838

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibit activity and may be useful in the diagnosis and/or treatment of capacity the activity and may be useful in the diagnosis and/or treatment of capacity the activity and may be useful in the diagnosis and/or treatment of capacity in the diagnosis and capacity i
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 353-354; 6221pp; English
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N-PSDB; AAK52970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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19-JUL-2000;
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-2000;
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20-OCT-2000;
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306 CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK
                                                                                                                             264
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, Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                             ---KKRTIIPTLV--
                                                                                                                                                                                                                          AKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIE-----
                                                                                                                                                                                                                                                                                                          SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGS--MCQRLRSMQYNGSYFDRG 210
                                                                                                                                                                                                                                                                                                                                                                             RQASLKKLAARQTRPVQPVAPRPEAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPKCQELRHLCDQFSAETARRRGLLSKSLELHRRLETSMKWCDEGIYLLASQPVDKCQSQ 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPKSVKLRAL-----RSPRKFGVAGRSCQ-----EVLRKGCLR--FQLPERGSRLCLYE 50
                                                                             RELENYTDCPELYGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE----
                                                                                                                                                                         ----ELLCVLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
                                                                                                                                                                                                                                                                              GGALRRGPYRRAKSEMSESRQGRGSAGEE--EESLAILRRHVMSELLDTER---AYVE--
                                                                                                                                                                                                                                                                                                                                                                                                                           PQVGL--IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGAEAALQEIEKFLETGAENKIQELNAIYKEYESILNQDLMEHVRKVFQKQASMEEVFHR 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL------SAFHE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0728422
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2000US-0693325.
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2000US-0620325.
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94.5; DI
Pred. No. 9.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous system
                                                                                                                        ----EAIKEQDGREVDWEYFYGLLFTSENLKLVHIV 305
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F, c
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                                                                                                                                                                                                                                                                                                                                                                          ----AKSPCPSPGIRRGSENS-SSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1152;
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g Qy

457

4 KPKSVKLRAL-----RSPRKFGVAGRSCQ----EVLRKGCLR--FQLPERGSRLCLYE 50

RPKCQELRHLCDQFSAEIARRRGLLSKSLELHRRLETSMKWCDEGIYLLASQPVDKCQSQ

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D X X P
                                                        Matches
                Query Match
Best Local
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                       Sequence
                                                                               Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer.
                                                                                                                                                                                                                                                                                 Claim 20; Page 3811-3813; 6221pp; English.
                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476283/51.
N-PSDB; AAK51986.
                                                                                                                                                                                                                                                                                                                                                                                           Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                        inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                         , Liu C,
, Wang D,
Yang Y,
               Similarity
                                                       1120 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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2000US-0598075.
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Wang J, Zi
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             5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Zhang
             Score 93.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                         Asundi V,
mang J. Re
                                                                                                                                                                                                                                                                                                                                                                                          Goodrich
 Mismatches
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                           DB
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  155;
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from
                           22;
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                           Length 1120;
                                                                                           (AAK52582) and 3666
the sequence listing
  Indels
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  99;
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Gaps
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   21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hamenostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                 WPI; 2001-442253/47.
N-PSDB; AAI59957.
                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001
Example 2; SEQ ID NO 5732; 10078pp; English
                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                    such as
                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                 (HYSE-)
                                                                                                                                                                                                                                 29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 5732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM40801 standard; Protein; 181 AA.
                                                                                                                                                                                                                                                                 L4-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725 RELENYTDCPELYGRCFLERMEDFQIYEKYCQNKPRSESLWRQCSDCPFFQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGS--MCQRLRSMQYNGSYFDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 PQVGL--IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                             Wang Z,
Zhou P,
                                                                                                                                                                                               HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHKKTTHKLNCDPSRIYKPQTRLKRKQPVRK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KKRTIIPTLV-----EAIKEQDGREVDWEYFYGLLFTSENLKLVHIV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGALRRGPYRRAKSEVSESRQGRGSAGEE--EESLAILRRHVMSELLDTER---AYVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGAEAALQEIEKFLETGAENKIQELNAIYKEYESILNQDLMEHVRKVFQKQASMEEVFHR 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQASLKKLAARQTRPVQPVAPRPEAL------AKSPCPSPGIRRGSENS-SSE 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGTELT-EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL------SAFHE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ELLCVLEGYAA-----EMDNPLMAHLLSTGLHNKKDVLFG--NMEEIYHFHNRIFL
                                                                                                                                                                                                                             ; 2000US-0488725.

2000US-0553317.

2000US-0598042.

2000US-0620312.

2000US-0662450.

2000US-0663450.

2000US-0693036.

2000US-0727344.
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                                                                                                                             Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                Chen R,
                                                                                                                                nen R, Ma Y,
{u C, Xue AJ,
Drmanac RT;
                                                                                                                                              Yang Y,
                                                                                                                                              Ren F, 1
Zhang J;
                                                                                                                                                             Wang D;
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RESULT 19
AAU03204
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Best Local
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                                            /label= OTHER
/note= "Other=
Misc-difference 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAA38642-AAA442213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
              Misc-difference
                                                                                                                     Misc-difference
                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                      Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                          apoptosia; programmed cell death; cancer; haematological di
bone marrow failure; myelodysplastic syndrome; aplastic ana
neutropaenia; leukaemia; cardiovascular disease; ischaemia;
                                                                                                                                                                                                                                                                                                                                           HLYAL47; CIDE; Cell death inducing DFF45-like effector; apoptosis; programmed cell death; cancer; haematologica
                                                                                                                                                                                                                                                                                                                                                                                             Human CIDE protein consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU03204 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.N.S disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                            reperfusion; liver disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU03204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 S----YPSTVGAEAQEEFLRVLGS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 RORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLR--EVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 PDFGPSSFVP------SWGATATGARKFLIAFN---INLLGTKEQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALHTVYEETC-REAQELSLPVVGS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AHRIALNLREQGRGKDQP---GRLKKVQGIGWYLDEKNLAQVSTNLLDFEVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDYFPS--VPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF--PE---RTCSQLQQADWA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                       Location/Qualifiers
/label- OTHER
                                                                                                                                   note= "Other= unknown"
                              note- "Other-
                                                                                                                                                         label- OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%; Sc
24.5%; Pr
ative 22;
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Pred. No.
                                unknown"
                                                                                unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
                                                                                                                                                                                                                                                                                                                                             cancer; haematological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .86;
                                                                                                                                                                                                                                                                                            neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
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PD XX PR XX PA
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ABG04580
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a CIDE (Cell death inducing DFF45-like effector) consensus sequence, thought to be involved in apoptosis and programmed cell death. Human HLYAL47 polypeptides (a CIDE B protein) and polynucleotides are useful in the treatment of cancer, haematological disorders, e.g., bone marrow failure including myelodysplastic syndromes aplastic anaemia, neutropaenia and leukaemia, cardiovascular diseases (e.g. ischaemia and reperfusion), liver diseases, inflammation and neurodegenerative pathologies. These may also be used as research reagents and materials for the discovery of treatments and diagnostics for animal and human diseases, for chromosome identification, as immunogens to produce HLYAL47 specific antibodies, and in screening for (ant)agonists of the HLYAL47 polypeptide.
                           Human; chromosome mapping;
                                                        Novel human
                                                                                      13-FEB-2002
                                                                                                                                              ABG04580 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New HLYAL47 polypeptides and polynucleotides, useful for treating cancer, hematological disorders, bone marrow failure such as myelodysplastic syndromes, aplastic anemia, neutropenia and leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grailhe P,
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular diseases
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            food supplement;
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                                                                                                                                                                                                                       104 EKGQSW 109
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                                                                                                                                                                                                                                                                                          14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL 72
                                                                                                                                                                                                                                                                                                                                        . Similarity
27; Conserv
                                                                                                                                                                                                                                                  TLGQAW 78
                                                                                                                                                                                                                                                                              RSSRK-GVTAASLQELLSKTLDTLVLXTGVVTLVLEEDGTAVDSEDFFQLLEDDTHLMVL 103
                                                                                                                                                                                                                                                                                                                                                                                                 221 AA;
                                                       diagnostic protein #4571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O'brien D;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99EP-0402926
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215..217
             medical
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                                                                                                                                                                                                                                                                                                                                                     5.2%;
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          imaging;
         gene mapping; gene therapy; forensi
maging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                       Score 93; DB 22; Length 221; Pred. No. 1.2; Indels
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                          forensic;
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Search completed: May Job time : 57 secs

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2003, 15:21:03

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                                                                                                                                                                                                                       cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc polynucleotides are also used in diagnostics as expressed sequence tags cf or identifying expressed genes. (I) is useful in gene therapy techniques cc to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or creations are useful in medical in a food supplement. (II) and its binding partners are useful in medical cc imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc and to produce other types of data and products dependent on DNA and can be consisted amino acid sequences of the invention.

Cc amino acid sequences. ABGOOQ10-ABG30377 represent novel human cc afternation, but was obtained in electronic format directly from WIPO case of the invention.
                                                                                                                                                 Matches
                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                          specification, at ftp.wimo in
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-639362/73.
106 EYFQALAGDTVFMVLQKGQKWQPPSEQGTRHPLSLSHKP 144
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:
                                                                                                                                                                  Similarity
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                                    DYFPSVPDNAELVLLTLGQAWQ-GYVSDIRRFLSAFHEP
                                                                          PKAPRARPCRVSTADRSVRK-GIMAYSLEDLLLKVRDTLMLADKPFFLVLEEDGTTVETE 105
                                                                                                         PKSVKLR-----ALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID No 34939; 103pp; English.
                                                                                                                                                                                                                         214
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                       Ã,
                                                                                                                                                                  5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
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                                                                                                                                                 16;
                                                                                                                                               Score 92.5; D
Pred. No. 1.2;
16; Mismatches
                                                                                                                                                                  1.2;
                                                                                                                                                 41;
                                                                                                                                                                                   22;
                                      95
                                                                                                                                                                                 Length
                                                                                                                                                 Indels
                                                                                                                                                                                   214;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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-Cg-cgn2_17USFTO_Spool/US09748451/runat_21052003_153829_16279/app_query.fasta_1.519
-DB-GenEmbl -CPMT-fastap -SUFFIX-rge -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blits -START-1 -END-1 - MARTIX-blosum62 -TRANS-human40.cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-20 -MODE-LOCAL
-OUTPMT-pcb -NORM-ext -HEAPSIZE-500 -MINLEUN-0 -MALIGN-20 -MODE-LOCAL
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-USER-US09748451_eCGN_1_1_2496_erunat_21052003_153829_16279 -NCPU-6 -ICPU-3
-NO_MMAP -LARCEQUERY -NEG_SCORES-0 -MAIT -DSPBJOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -MARN_TIMEOUT-30 -THREADS-1 -XGAPODP-10 -XGAPEXT-0.5 -FGAPOP-6
-DEVENT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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-MODEL=frame+_p2n.model -DEV=xlh
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1: gb_ba:
2: gb_htg
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29: em_vi:*
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36: em_htg_vrt:*
37: em_htg_vrt:*
39: em_htg_ohum:*
40: em_htgo_hum:*
41: em_htgo_mus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

410 355.5 329.5 321 320 320 295 295 294 1124.5 1109.5 1108.5 1108.5 1106.5 1106.5 1106.5 1106.5 1106.5 1106.5 Query Match 100.0 100.0 100.0 99.8 1316 15585 142970 1499 1159 160716 1833 4339 2118 211505 197159 2615166 18766 1851 1851 1851 1851 1438 DB AK098413 AF1426316 AF149797 AB036773 AL806525 AC009340 AE003636 AC012906 HSVIMENTA PSAJ2156 PSAJ2156 AF136601 Ħ AB028912 Homo sapi E36548 Caspase-act E36551 Caspase-act AB009377 Mus muscu AF136598 Rattus no AL353671 Human DNA AL353671 Homo sapi AF406761 Gallus 91 AF406761 Gallus 91 AF406761 Jenno sapi AK098413 Homo sapi AK098413 Homo sapi AF426316 Danio rer U05823 Mus musculu AJ002156 Pinus str AF136601 Rattus no AE002394 Neisseria Continuation (23 o AL512293 Leishmani AL162758 Neisseria AX044029 Sequence AF03268 Oryza sat AC124011 Mus muscul M20384 Sus scrofa M22647 Pig apolipo X96391 H.sapiens m M25246 Human vimen AF149797 Drosophil AB036773 Drosophil AL806525 Mus muscu AC009340 Drosophil AE003659 Drosophil AC012906 Drosophil AC012906 H.saplens v BC030573 Homo sapi AL603906 Human DNA AB013918 Homo sapi AR122560 Sequence AF064019 Homo sapi Description AF409062 Homo Homo sapi Homo sapi Homo sapi Homo

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                                                                                GTGGCTGGCCGGAGCTGCCAGGAGGTGCTGCCCAAGGGCTGTCTCCGCTTCCAGCTCCCT
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                         GAGCGCGGTTCCCGGCTGTGCCTGTACGAGGATGGCACGGAGCTGACGGAAGATTACTTC
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ESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLC
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                                                      281 GlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLys 300
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutexternative Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2839)

Liu,X., Li,P., Widdlak,P., Zou,H., Luo,X., Garrard,W.T. and The 40-kba subunit of DNA fragmentation factor induces DNA fragmentation and chromatin condensation during apoptosis fragmentation and chromatin condensation during apoptosis fragmentation and Sci. U.S.A. 95 (15), 8461-8466 (1998)
Similarity:
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2 (bases 1 to 2839)
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AQQILCDEGAPGRORILADILHNYSQNIAAETRAEDPWEGGIESRPGSKSGYIRYSC
ESRIRSYLAEVSSYPSTYGAEAGEEFLAVLGSMCQRIRSMCYNGSYFDRGAKGGSRIC
TPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI
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/db_xref="taxon:9606"
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/product="DNA fragmentation factor 40 kDa subunit"
/protein_id="AAC39920.1"
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/function="nuclease;
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/db_xref="GI:3347857"
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hromatin condensation during apoptosis"
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                                                                    Homo sapiens caspase-activated n
AF039210
AF039210.1 GI:3056726
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1017)
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Williams,L.T.
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Horton Street, Emeryville, CA 94608, USA
Location/Qualifiers
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RKRQ"
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/protein_id="AAC39709.1"
/db_xref="G1:3056727"
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/db_xref="taxon:9606"
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                                                                                  Direct Submission
Submitted (GF-JUN-1999) Akira Nakagawara, Chiba Cancer Center Research Institute, Division of Biochemistry; 666-2 Nitona, Chubh-ku, Chiba, Chiba 260-8717, Japan (E-mail:akiranakehiba-cp.pref.chiba.jp. Tel:81-43-264-5431(ex:5201), Fax:81-43-265-4459)
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 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Neuroblastoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                                                           21 ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF409060 1028 bp mRNA linear (PRI 11-SEE-Homo sapiens DNA fragmentation factor B truncated form I (DFFB) mRNA, complete cds, alternatively spliced.

AF409060
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Submitted (13-AUG-2001) Ciencies
Lleida, Av. ROVITA ROUTE 44, Llei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comella, J.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeu
                                                                                                                                                                                                         MetLeuGlnLysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGly
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                                         GTGGCTGGCCGGAGCTGCCAGGAGGTGCTGCGCAAGGGCTGTCTCCCGCTTCCAGCTCCCT 124
                                                                                                                                                                              ATGCTCCAGAAGCCCAAGAGCGTGAAGCTGCGGGGCCCTGCGCAGCCCGAGGAAGTTCGGC
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/protein_id="AAL02005_1"
/protein_id="AAL02005_1"
/db_xref="GI:1553729"
/translation="MLQKFKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGS
/translation="MLQKFKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGS
RLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGCGRCERHQALPQCISRATGGAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell
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/db_xref="taxon:9606"
/cell_line="IMR-5"
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218 sThrProGluGlyTrPPheSerCysGlnGlyProPheAspMeLAspSerCysLeuSerAr
218 sThrProGlnGlyTrPPheSerCysGlnGlyProPheAspMeLAspSerCysLeuSerAr
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218 sThrProGlnGlyTrPheSerCysGlnGlyProPheAspMeLAspSerCysLeuSerAr
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218 sThrProGlyTrPPheSerCysLeuSer
218 sThrPro
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Lleida, Av Rovira Roure
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Bayascas, J.R., Yuste, V.J.,
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/protein_id="AAL02006.1"
/db_xref==0(1:1553,731"
/translation="MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGS
/translation="MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGS
RICLYEDGTELFEDYFFSVPDNAELVLLTLGQAWQGCEWQGLWRCERHQALPQCISRA
TGGAHPGRPAAAV"
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/db_xref="taxon:9606"
/cell_line="IMR-5"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Comella, J.X., Bayascas, J.R.,
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ted (13-AUG-2001) Ciencies Mediques Basiques,
t, AV. ROVITA ROUTE 44, Lleida 25198, Spain
         /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="IMR-5"
/cell_type="neuroblastoma"
1. 1071
                                                                                                        Cocation/Qualifiers
                                                                                                                                                                                                                                                                               Eutheria;
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204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                               484 GGCTTGGAGTCCCGATTTCAGAGCAAGTCTGGCTATCTGAGATACAGCTGTGAGAGCCGG 543
                                                                                                                                                                                                                                                                                                                                                                                             124 HisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProProTrpPheGlu 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe
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3 306 c 319 g 204 t
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/note="CIDE-N-only protein; alternatively spliced"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-JUN-1999) Akira Nakagawara, Chiba Cancer Center Research Institute, Division of Blochemistry; 666-2 Nitona, Chubh-ku, Chiba, Chiba 260-8717, Japan (E-mail-akiranakéchiba-cc.pref chiba.jp, Tel:81-43-264-5431(ex.5201), Fax:81-43-265-4459)
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3008 bp mRNA linear [PRI 03-APR-2001]
Homo sapiens DFF40 gamma mRNA for DNA fragmentation factor 40 kDa
subunit gamma, complete cds.
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DFF40 gamma; DNA fragmentation factor 40 kDa subunit gamma; Homo sapiens tissue_lib:testis cDNA to mRNA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 GAAACGCACCATCATTCCTACACTGGTGGAAGCAATTAAGGAACAAGATGGAAGAAGT
                                                                                                   CAGTAACAGGGAGGAGCAGCATCCTCTTCAGCACCTGGAACCTGGATCACATAATAGAAAA
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OS Homo sapiens (human)
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1 (bases 1 to 1038)
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C12N15/09,C07K16/40,C12N5/10,C12N9/22,C12N15/00,C12N5/00
Key
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OS HOMO SAPIENS (human)
PN JP 199233495-A/1
PD 17-SEP-1993
PF 25-DEC-1998 JP 1983
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PC C12P21/08//(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12P21/02, PC C12R1:19),
PC C12N15/00,C12N5/00,(C12N15/00,C12R1:91)
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1038)
Shigekazu,N. and Masato,E.
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                                                                                                 SHIGEKAZU NAGATA, MASATO ENARI
C12N15/09,C07K14/81,C07K16/18,C12N1/21,C12N5/10,C12N9/99,
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                                                                                                                                                                                                                                                                                                                               161 GluSerArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAla 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAla 120
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                               490 GAGAGTCGGATCCGGGGTTACCTAAGAGAGGTGAGCGCTTACACCTCTATGGTGGATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 GATCTTCTGCATCACGTGAGCCAGAATATTACTGCAGAGACCCGGGAGCAGGACCCATCC
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       School, B-
565-0871,
                                                                                                                                                                                                                                                                                                                                                                     565-8871, Japan (E-mail:nagata@genetic.med.osaka-u.ac.jp, Tel:81-6-879-3310, Fax:81-6-879-3319)
On Aug 31, 1998 this sequence version replaced gi:2913870 Sequence updated (24-Feb-1998)
Sequence updated (29-Aug-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (sites)
Sakahira.H., Enari,M. and
Cleavage of CAD inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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Mammalia; Eutheria;
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CAD.
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/product="CAD"
/product="CAD"
/protein_id="BAA24977.1"
/protein_id="BAA24977.1"
/db_xref="GI:2913871"
/dr_xref="GI:2913871"
/dr_xref="GI:2913871"
/dr_xref="GI:29
                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="WR19L"
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Rattus norvegi
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24 GTGCTCCCCCAACCCAAATGCGTCAAGTTGCGAGCTCTACACAGCTCGTGCAAGTTCGGC 83
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Submitted (23-MAR-1999) Department of Neurology, BST, Pittsburgh University Medical School, 3500 Terrace Str Pittsburgh, PA 15213, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao,G., Pei,W., Lan,J., Stetler,R.A., Luo,Y., Nagayama,T., Graham,S.H., Yin,X.M., Simon,R.P. and Chen,J. Caspase-activated DNase/DNA fragmentation factor 40 mediates apoptotic DNA fragmentation in transient cerebral ischemia and
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J. Neurosci. 21 (13), 4678-4690 (2001)
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PGSRLCMYEDGTEVUDDCFPSLPNDSELLLITAGETWHGYVSDITRLLSVFUNEPHAGV
IQAARQLLSDEQAFLRGKLLADLLHHVSQNITAETPERDDDSWFEGLESBERNKGGYLR
YSCESRIRGYLREVSAYISMVDAAARBEYLRVLSSMCHKLKSVQYNGSYFDRGAEASS
RLCTPEGWFSCQGFPDLESCLSKHSINFYGNRESRILFSTMNLDHIIEKKRTVFFTLA
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s AL353671 15585 bp DNA linear PRI NITION Human DNA sequence from clone RP11-205M20 on chromosome sequence.

SSION AL353671 GI:16304896
DRDS HTG.

21-OCT-2001 9, complete

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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    61
                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-205M20 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-205M20 is at 155585 in this sequence. The true left end of clone RP11-555J4 is at 84490 in the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP SHISSPROT; TREMBL; Wp:, WORMPEP; Information on the WORMPEP bith. //www.sanger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
On Oct 21, 2001 this sequence version replaced gi:15021313.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence. The true left end of clone RP11-5554 is at 84490 in sequence. The true right end of clone RP11-334P12 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9 constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RP11-205M20 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bray-Allen,S.
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                                                                                                                                             ValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuPro 40
                                                                  GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe
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Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                            AL355811 142970 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 9 clone RP11-562A11 map pl3.1-21.1, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.
                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                   HTG; HTGS_PHASE1;
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Sequencing vector: plasmid; LOB752; 100% of rea
Chemistry: Dye-terminator ET-amersham; 18% of r
Dye-terminator Big Dye; 81% of reads
Consensus quality: 127694 bases at least Q40
Consensus quality: 13388 bases at least Q20
Consensus quality: 13588 bases at least Q20
Insert size: 140470; sum-of-contigs
Insert size: 155298; 6.6% error; agarose-fp
Quality coverage: 3.12x in Q20 bases; sum-of-co
coverage: 3.39x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 4033: contig of 4033 bp in length
4034 4133: gap of 100 bp
4134 8168: contig of 4035 bp in length
8169 8268: gap of 100 bp
14731: contig of 6463 bp in length
14732 14831: gap of 100 bp
14832 18803: contig of 3972 bp in length
1804 18903: gap of
75880 75979 gap of 75978 75980 75979 gap of 75980 75979 gap of 7598 bp in length 81018 81117; gap of 100 bp 1118 95015; contig of 13898 bp in length 95116 95115; gap of 100 bp 95116 9580; contig of 4565 bp in length 9581 99780; gap of 100 bp 104231 104230; gap of 100 bp 104231 10424; contig of 4350 bp in length 110143 110244; gap of 100 bp 110245 115096; contig of 4852 bp in length 115097 115196; gap of 100 bp 115097 115196; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39612 39711: gap of 100 bp 11 length 1838 48437; gap of 100 bp 10 length 1838 48437; gap of 100 bp 100 bp 100 length 1838 50511: gap of 100 bp 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 50512 5
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26248 26347: gap of 100 bp
26348 30120: contig of 3773 bp in length
30121 30220: gap of 100 bp
30221 3020: gap of 100 bp
30221 32461: contig of 2241 b-
32462 32561: gap of
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.18258 118357: gap of 100 k
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59567. .64909
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/note="assembly_fragment:00027
fragment_chain:3"
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75980. .81017
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fragment_chain:2"
18904..21145
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          note="assembly_fragment:01269"
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126738. .132827
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L15197. .118257
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104231...110144
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59906. .75879
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ragment_chain:2"
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.4832. .18803
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5010. .69805
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6348. 30120
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42970: contig of 10043 bp in length
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Samejima, K., Tone, S. and Earnshaw, W.C.
CAD/DFF40 nuclease is dispensable for high molecular weight
Cleavage and stage I chromatin condensation in apoptosis
J. Biol. Chem. 276 (48), 45427-45432 (2001)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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ArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGln
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Danio rerio caspase-activated DNase mRNA,
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Danio rerio

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1. (bases 1 to 1159)
                                                                                                                         Submitted (10-JUL-2000) Institute Sinica, 128, Yen-Chiu-Yuan Road, S
                                                                                                                                                                              Liu,
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                                         /organism="Danio rerio"
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                                   243 ProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIle
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                                                                                                                                                                                                                                                                                                                              164 IleArgSerTyrLeuArgGluValSerSerTyrProSerThrVal---GlyAlaGluAla 182
                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AGTAACCTGAGGGACCGTTCAGAGCTGGAGAACAGACTACAGGATCATGACTGGTTTGAA
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                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator; 2% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Consensus quality: 158827 bases at least Q40
Consensus quality: 159096 bases at least Q30
Consensus quality: 159180 bases at least Q20
Insert size: 160716; sum-of-contigs
Insert size: 160784; 0.4% error; agarose-fp
Quality coverage: 10.84x in Q20 bases; sum-of-contigs Quality
coverage: 10.19x in Q20 bases; agarose-fp
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Homo sapiens chromosome 1 clone
PROGRESS ***, in ordered nicon-
AL691572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: Web site: htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 160716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name:
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the accession number will be preserved.
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                 clone_end:T7
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                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                note="assembly_fragment:03871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens cDNA FLJ25547 fis, AK098413
                                                                                                                                                    NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA library sequencing Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Hum
                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-JUI-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1833)
Sugano, S. and Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo capping; fis (full insert sequence). Homo saplens thyroid cell_line:JCR cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA sequencing project
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                                                                                                            ne Center; 3'-end one pass sequencing: RAB;
insert sequencing: RAB and Helix Research 1
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                                                                                    Location/Qualifiers
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Primates;
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ORIGIN
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Local Similarity:
Query Match:
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444 c 440 g 461 t
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Search completed: May 26, 2003, 16:20:42 Job time: 3232 secs

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re greater than or equal to the score of the result being printed,
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Sequence 1195, Appl
Sequence 11, Appl
Sequence 15, Appl
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US-09-843-676-217	US-09-050-516-42	US-10-278-547-42	US-10-053-753-2	US-09-853-625B-11	US-09-801-368-370	US-10-197-666A-102	US-09-799-875-17	US-10-197-666A-104	US-09-800-729-206	US-09-987-107-37	US-10-197-666A-48	US-09-925-300-1664	US-09-950-046A-2	US-09-820-843A-58	US-10-003-496-6	US-10-120-687-1	US-10-136-891-2	US-09-963-875-1	US-09-859-888-5	US-09-772-316-2	US-10-118-328-5	US-10-151-193-5	US-10-151-193-6	US-10-097-340-18	US-10-097-340-19
		Sequence 42, Appl	~	Sequence 11, Appl	_		Sequence 17, Appl	Sequence 104, App	Sequence 206, App	Sequence 37, Appl	Sequence 48, Appl	Sequence 1664, Ap	Sequence 2, Appli	Sequence 58, Appl	е 6	Sequence 1, Appli	Sequence 2, Appli	1,	Sequence 5, Appli	Sequence 2, Appli	5		Sequence 6, Appli	18,	Sequence 19, Appl

ALIGNMENTS

MESULT 1 US-09-748-451-2 ; Sequence 2, Application US/09748451 ; Patent No. US20010011078A1

GENERAL INFORMATION:

APPLICANT: WANG, XIAODONG
APPLICANT: LIU, XUESONG
TITLE OF INVENTION. DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
FILE REFERENCE: UTSD:546USD1
CURRENT APPLICATION NUMBER: US/09/748,451
CURRENT FILING DATE: 109/061,702
PRIOR APPLICATION NUMBER: 09/061,702
PRIOR FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 338
Type: Patentin Ver. 2.1
ORGANISM: Homo sapiens ρ QΥ 밁 밁 Q 밁 밁 Query Match 100.0%; Score 1789; Best Local Similarity 100.0%; Pred. No. 8 Matches 338; Conservative 0; Mismatches 121 DLLHNYSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTYGA 180 181 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS 241 INPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLK 300 181 EAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHS 240 121 DLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGA 180 61 61 PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120 1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60 PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60 0; Mismatches 8.3e-158; 0; Length 338; Indels 0; Gaps

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               Sequence 12, Application US/10242943 Publication No. US20030087412A1 GENERAL INFORMATION:
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LENGTH: 76
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TITLE OF INVENTION:
TITLE OF INVENTION:
ITLE OF INVENTION:
ILE REFERENCE: 35800
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Publication No.
   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/185,609
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                                                                                                                                                                                                                                                                                                           ery Match
                                                                                                                                                                                                                                                                                                                                               PEATURE:
OTHER INFORMATION: Consensus sequence for the -165-800-13
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Nandabalan, Krishnan
                                                                                                                                        ALEQGEKW 76
                                                                                                                                                                                                        RNVRK-GVAASSLEELLSKYLDKLKLPDSLEPVTLVLEEDGTEVEDEEYFRTLPNNTELV
                                                                                                                                                                                                                                        RSPRKFGVAGRSCQEVLRKGCLRFQLPE--RGSRLCLYEDGTEL-TEDYFPSVPDNAELV 70
                                                                                                                                                                      LLTLGQAW 78
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Meyers, Rachel E.
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                                                                                                                                                                                                                                                                          6.4%; Score 114; DB 9; Length 76;
44.1%; Pred. No. 0.0023;
Live 12; Mismatches 22; Indels
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; ORGANISM: Mus
US-10-152-647-4
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US-10-152-647-4
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: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-242-943-12
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                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                           SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10152647
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                                                              Matches
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Best Local Similarity 20.8%;
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/152,647
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/610,401
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MORISHIMA, NO. US20020137110A1uhiro,
APPLICANT: NAKANISHI, Keiko,
APPLICANT: SHIBATA, Takehiko
TITLE OF INVENTION: Antibody against cleavage product of vimentin
FILE REFERENCE: 522.1004
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                                                                                                                                                                                                                                             SOFTWARE: PatentIn
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
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                                                                                                                                                                                                    LENGTH: 466
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27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86 ::::| | | | | | | | | | | : : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
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                                                              Conservative
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20.1%;
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                                                          Score 99; DB 12; Length 46; Pred. No. 0.69; Indels 113; Indels
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Pred. No. 0.69;
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                                                            Gaps
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; ORGANISM: Shigella Flexneri
US-10-043-487-302
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TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
TITLE OF INVENTION: Manmalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR PRILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patentin version 3.1
SEQ ID NO 302
LENGTH: 405

TENGTH: 405

TENGTH: 405
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Rest Local Similarity 20.8%;
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APPLICANT: Pierre, LE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 EDIMR----LREKLQEE-----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 170
                                                                                                                           329 KMALDIEIATYRKLL---EGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTF---L
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                        383 IKTVETRDGQVIN 395
                                                                           273 VEAIKEQDGREVD 285
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                                                                                                                                                                           QGPFDMDSCLSRHSINPYSNRESRIL----FST----WNLDHI----IEKKRTIIPTL 272
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o. US20030055220A1
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-642-3
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US-09-935-642-3
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US-09-923-779-155
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Publication No. US20030044795A1
GENERAL INFORMATION:
APPLICANT: BYRJALSEN, Inger
APPLICANT: LARSEN, Peter
APPLICANT: STEPHEN, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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Best Local Similarity
Matches 65; Conserv
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
                                                                                                                                                                                                                                                                                                          Sequence 155, Application US/09923779 Patent No. US20020076721A1
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: PCT/GB97/02394
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: PCT/GB9707132.8
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: PCT/GB9618600.2
PRIOR FILING DATE: 1996-09-06
                                                                           APPLICANT: Pyle, Ruth A.
APPLICANT: Xi, Jiangchun
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
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TITLE OF INVENTION: Biochemical Markers for the Human
TITLE OF INVENTION: Endometrium
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US-10-152-647-3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/152,647
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/09/610,401
PRIOR FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIBATA, Takehiko TITLE OF INVENTION: Antibody against cleavage FILE REFERENCE: 522.1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MORISHIMA, NO. US20020137110Aluhiro, APPLICANT: NAKANISHI, Keiko, APPLICANT: SHIBATA, Takehiko
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TYPE: PRT
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RGANISM: Homo sapiens
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                                        YKSKFADLSEAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                               EDIMR---LREKLQEE----MLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
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20.8%;
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US-10-165-800-14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. US20030092116A1el Nucleic Acid Sequences Encoding TITLE OF INVENTION: Adenylate Kinase, phospholipid Scramblase-Like, DNA TITLE OF INVENTION: Fragmentation Factor-Like, Phosphatidylserine Synthase-Like, TITLE OF INVENTION: and ATPase-Like Molecules and Uses Therefor
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FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/181,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/781,677 FILING DATE: 2001-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/795,038
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                                                                            108
                                                                                                               103 EQGQSWSPKSGMLSYGLGREKPKHSKDIARITFDVYKQNPRDLFGSLNVKATFYGLYSMS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 QGPFDMDSCLSRHSINPYSNRESRIL-----FST-----WNLDHI----IEKKRTIIPTL 272
                                                                                                                                                         73
                                                                                                                                                                                           45 RTVRK-GLTAASLQELLDK-VLETLLLRGVLTLVLEEDGTAVDSEDFFQLLEDDTCLMVL 102
                                                                                                                                                                                                                                14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LING DATE: 2001-02-
                                                                                                                                                                                                                                                                        46;
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                                                                                                                                                                                                                                                                                          Similarity
                                      CDFQGVGPKRVLRELLRGTSSQL---
                                                                        CDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIR 165
                                                                                                                                                       TLGQAW---QGYVS---
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Kapeller-Libermann, Rosana
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25.8%;
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                                                                                                                                                                                                                                                                    Score 91; DB 9
Pred. No. 1.4;
21; Mismatches
                                                                                                                                                     -DIRRFLSAFHEPQ------VGLIQAAQQLL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0
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                                      -QGLGHMLLGISSTLRHVVEGADR 208
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US-09-748-451-4
; ORGANISM: Rattus norvegicus US-10-086-135-3
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US-10-086-135-3
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ORGANISM: Homo sapiens
US-09-748-451-4
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Best Local :
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APPLICANT: LIU, XUESONG
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
FILE REFERENCE: UTSD-546USD1
CURRENT APPLICATION NUMBER: US/09/748,451
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION UNMER: 09/061,702
PRIOR APPLICATION UNMER: 09/061,702
PRIOR APPLICATION UNMER: 09/061,702
PRIOR PILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTING DATE: 1998-04-16
LENGTH: 331
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/086,135

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/366,448

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/095,199

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 35

SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PANCREATIC AND OVARIAN POLYPEPTIDE TITLE OF INVENTION: ZSIG58
                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 98-24
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                                                    TYPE: PRT
                                                                          LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 YFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 QSCATV-QRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQE---ESKAAFGE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFD- 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 IVDDDDYFLCLPSNTKFVALASNEKW------AYNNSDGGTAWISQESFDVDET 116
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Similarity 22.2%;
78; Conservative 4
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; Pred. No. 3.7;
49; Mismatches 146; Indels 78;
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US-09-925-300-1495
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US-09-925-300-1495
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1495
LENGTH: 366
TYPE: PRT
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Best Local Similarity 21.8%; Pred. No. 5.
Matches 60; Conservative 40; Mismatche
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/U500/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION UNMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                               152 DSGAGLKWKNVARQLKEDLSSIILLSEEDLQMLVDAPCSDLAQE------LRQSCATV 203
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246 ---ESKAAFGEEVDAVDTGISRET-----SSDVALAS----HIL----
                                                  222 GWFSCQGPFD-----MDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI 276
                                                                                                       204 QRLQHTLQQVLD-----QREEVR-----QSKQLLQLYLQALEKEGSLLSKQE 245
                                                                                                                                                          163 -RIRSYLREVSSYPSTYGAEAQEEFLRYLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPE 221
                                                                                                                                                                                                                                                                     109 DEQAPQRQRLLADLLHNVSQNIAAETRAE-----DPPWFEGLESRFQSKSGYLRYSCES- 162
                                                                                                                                                                                                                                                                                                                       104 IVDDDDXFLCLPSNTKFVALASNEKW------AYNNSDGGTAWISQESFDVDET 151
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                                                                                                                                                                                                                                                                                                                                                                                                                               45 PESGEIRTLKPCLLRRNYSREQHGVAA-SCLEDLRSKACDILAIDKSLTPVTLVLAEDGT 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 87; DB 10; Length 366; 22.4%; Pred. No. 6.4; ative 50; Mismatches 131; Indels 100;
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5.7;
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SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/165,800
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/790,179
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                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/795,038 FILING DATE: 2001-02-26
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211 QQKGRLHSY 219
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                                                                                                                                           QSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPRDLFGSLNVKATFYGLYSM 162
                                                                                                       LCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCE----
                                                                       SCDFQGLGPKKVLRELLRWTSTLL-
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Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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LENGTH: 219
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                                                                      APPLICANT: COLLINS, James E.
APPLICANT: FAABERG, Kay S.
APPLICANT: ROSSOW, Kurt D.
TITLE OF INVENTION: PROCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 110.01250101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 35800/247838
CURRENT APPLICATION NUMBER: US/10/165,800
CURRENT FILING DATE: 2002-06-07
                                     CURRENT APPLICATION NUMBER: US/10/203,224
CURRENT FILING DATE: 2002-08-07
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TITLE OF INVENTION:
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FILING DATE:
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FILING DATE: 2001-02-21
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TE: 2002-08-07
NUMBER: PCT/US01/04351
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RESULT 16
US-10-143-849-2
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PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/193,220
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/206,624
PRIOR PRILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/215,373
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR APPLICATION NUMBER: 60/260,041
PRIOR PILING DATE: 2001-01-05
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Matches 64
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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ENGTH: 1458
                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/143,849
FILING DATE: 14-May-2002
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genetic control of flowering
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
CARDESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. US20030074699Alth Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Coupland, George M.
Putterill, Joanna J
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/516,191
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/945,056
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 IEAGRQLV-----PNRDRILAALAYHMKAQNASEYYASAAAILMDSCACIDHDPEWYEDL 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 RLRSMQYNGSYFDR-----GAKGGSRLCTPEGWFSCQGPF-----DMDSCLSRHSIN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ---ESRFQSKSGY-----LRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLG-SMCQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 PLLPTCKDINMVKVACNVLLSKFIVGPPGSGKTTWLLGQVQDDDVIYTP 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 GLLFTSENLKLVHIVCH------KKTTHKLN--CDPSRIYKP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 PPRTVIMKVGNKTTALDPGRYQSRRGLVAVKRGIA------GNEVDLSDGDYQVV 763
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STATE: Virginia
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nilarity 22.1%;
Conservative 3
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Pred. No. 59;
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TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-143-849-2
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US-10-051-311A-2
Sequence 2, Application US/10051311A
Patent No. US20020164620A1
Patent No. US20020164620A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim International GmbH
TITILE OF INVENTION: Method for identifying compounds that modulate sister
TITILE OF INVENTION: Chromatid separation
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                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 2120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-051-311A-2
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Matches
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                                                                                                                                                                                              Query Match
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PRIOR FILING DATE: 2001-66-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2002-06-20
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR EILING DATE: 2001-01-19
                                                                                                                                                                              Local
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NAME: MS Mary J Wilson
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 SGYLRYSCESRIRSYLREVSSYPSTYGAEAQEEFLRYLGSMCQRLRSMQYNGSYFDRGAK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GGSRLCTPEGWFSCQGPFDMDSCLSR-HSINPYSNRESRI------LFSTWNLDHIIE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 SSMDYKFTGEYSQHQQNCS-----VPQT 206
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                                                                              197 RAVAAHQLFDASGHGLNEADADFLDDLLSRHVIRALVGERGSSSGLLSPQRALCLLE--- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 SAYLCMSCDAQVHSANRVAS----- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 -- AFLCEADDASLC-----TACDSEVHSANPLARRHQRVPILPISGNSFSSMTTTHHQS 123
                                      54 ELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFL-SAFHEPQVGLIQAAQQL----- 106
                                                                                                                    11 RALRSPRKFGVAGRSCQE------VLRKGCLRFQLPERGS-----RLCLYEDGT 53
                                                                                                                                                             66;
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9422083.7 FILING DATE: 02-NOV-1994
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                                                                                                                                                             Conservative
                                                                                                                                                           4.6%; Score 83; DB 9; Length 2120;
18.8%; Pred. No. 1.7e+02;
ative 52; Mismatches 130; Indels 104; Gaps
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  -LTL-----EHCRRFCWSRHHDKAISAVEKAHSYLRNTNL 287
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Pred. No. 11
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                                                                                                                                                                                                   Length 2120;
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RESULT 19
US-10-097-340-23
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; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Wherein Xaa may be any one of Leu
US-09-867-550-1316
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 Sequence 23, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
APPLICANT: John MONAHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1316
LENGTH: 277
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CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leach, Martin D. APPLICANT: Mehraban, Fuad, APPLICANT: Conley, Pamela APPLICANT: Law, Debbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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No. US20020082206A1
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                                                                                                                                                                            306 CHKKTTHKL 314
                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                   165 RSYLREVSSYPSTYGAEA-----QEEFLRYLGSMCQRLRSMQYNGSYFDRGAKGGSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 QFFLSGLERGTKRRY------RLDAILSLFAFLGGYCSLLQQLRDDGVY---GGS
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                                                                                                                                                                                                                                               KRTIIPTLVEAIKEQDGR-----
                                                                                                                                                                                                                                                                                                                  CTPEGWFSCQ--GPFDMDSCLSRHSINPYSNRESRILFSTWNLDHII------EK
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                                                                                                                                           ---KKDHQL 174
                                                                                                                                                                                                            QATLESAELEAAQEAGAQPPPSQSQDKDMKKKKMKESEADSEVKHQPIFIKERLKLFEIL
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                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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Matches
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LENGTH: 633
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Assessment,
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FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/324,967
                                  302 VHIV 305
                                                                   338 KPSLGWLQSAYKEFDRKDGDLTMWPRLVSNSKLKRSSHLSLPKYWDYRY-----KKNLKA 392
                                                                                                     266
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393 LYVV
                                                                                                                                                                      214 -GSRLCTPEGWFSC-----QGPFDMDSCLS--RHSINPYSNRESRILFSTWNLDHIIEKK 265
                                                                                                                                                                                                         225 THSCILELQRDKAAAAAVLGAVRKRPSVVPMAGQDPALSTSHPFYDVARHGILQVAGDDR 284
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                                                                                                                                      FGRRVVT----FSCCRMPPSHELDHQRLLEYLKYTLDQYVENDYTIVYFHYGLN---SRN
                                                                                                                                                                                                                                             -----EFLR------VLGSMCQRLRSMQYNGS-----YFDRGAKG-----
                                                                                                                                                                                                                                                                               HARVPPAIVQMLLVLQGVHESRGVTEDYLR--LETLVQ----KVVSPYLGTYGLHSSEGPF
                                                                                                                                                                                                                                                                                                              RAEDPP-----WFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQE---
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                                                                                                                                                                                                                                                                                                                                                                                                                     FSLNEGVRQLLKTELGSFFTE-YLQNQLLTKGMVILRDKIRFYEGQKLLDSLAETWDFFF
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Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Shubhangi KAMATKAR
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Robert C. BAST,
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                 -LLHFRNAITLSVKLEDALARA 169
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                                                                                                   -WEYFYGLLFTSENLKL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-10-097-340-19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
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TYPE: PRT
ORGANISM: Homo sapiens
0-097-340-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-03-14
APPLICATION NUMBER: 60/325,149
FILING DATE: 2001-09-26
APPLICATION NUMBER: 60/276,026
FILING DATE: 2001-03-14
APPLICATION NUMBER: 60/324,967
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FILING DATE: 2001-08-10
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                                                                                                                                                                                           170 HARVPPAIVOMLLVLOGVHESRGVTEDYLR--LETLVQ---KVVSPYLGTYGLHSSEGPF 224
                                                                                             225 THSCILELQRDKAAAAAVLGAVRKRPSVVPMAGQDPALSTSHPFYDVARHGILQVAGDDR 284
                                                                                                                                                                                                                                           135 RAEDPP-----WFEGLESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQE--- 184
                                                                                                                                                                                                                                                                                           124 SDVLPMLQAIFYPVQGKEPSVRQLA-------LHFRNAITLSVKLEDALARA 169
285 FGRRYVT----FSCCRMPPSHELDHQRLLEYLKYTLDQYVENDYTIVYFHYGLN---SRN 337
                                                214 -GSRLCTPEGWFSC-----QGPFDMDSCLS--RHSINPYSNRESRILFSTWNLDHIIEKK 265
                                                                                                                                          185 -----EFLR------VLGSMCQRLRSMQYNGS------YFDRGAKG------ 213
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                                                                                                                                                                                                                                                                                                                                        83 SDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLLH------NVS-QNIAAET 134
                                                                                                                                                                                                                                                                                                                                                                                        65 FSLNEGVRQLLKTELGSFFTE-YLQNQLLTKGMVILRDKIRFYEGQKLLDSLAETWDFFF 123
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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Robert C. BAST, Jr.
Karen LU
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Karen GLATT
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Title:
Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
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5.5
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Gapop 10.0 , Gapext 0.5
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1789
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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                US-09-085-199B9
US-09-085-7-095-33
US-08-157-005-3
US-08-177-085-3
US-08-177-085-3
US-09-165-864-3
US-09-165-864-3
US-09-165-256-2
US-09-165-23-16
US-09-165-023-16
US-09-165-023-16
US-09-165-023-31
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US-09-610-401-4

US-09-610-401-3

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US-08-847-900-3
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Sequence 4, Appli
Sequence 3, Appli
Sequence 18, Appl
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Sequence 32, Appli
Sequence 3, Appli
Sequence 3, Appli
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Matches Query Match

Local Similarity

100.0%; Score 1789; 100.0%; Pred. No. 36

9; DB 4; 3e-183; 0,

Length 338; Indels

0;

Gaps

Conservative

0;

Mismatches

TOPOLOGY: US-09-061-702-2

STRANDEDNESS:

linear

TELEPHONE: (512)474-7577
TELEPAX: (512)474-7577
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids

2:

REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION:

P-43,363

UTSD:546

APPLICATION NUMBER: US/09/ FILING DATE: CONCURRENTLY CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: MCMILLIAN, Nabeela R REGISTRATION NUMBER: P-43,

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61 PSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLA 120

1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60

RESULT 1 Sequence 2, Sequence 2, Ratent No. GENERAL IN APPLICAN CORRESPON ADDRES STRET COURTES CO	2220000000000000000000000000000000000
702- 0 2/ 0 0F 0 OF	81.5 81.5 81.5 81.6 81 81 81 81 81 81 81 80.5 79.5 79.5 79.5 79.5 79.5 78.5
HORMATION: 6165737 G165737 T: Wang Xia T: Liu Xues TINVENTION: F SEQUENCES: INVENTION: F SEQUENCES: INDERES SEE: Arnold, F P.O. BOX 4 HOUSTON TX TYPE: Flopp FER: IBM PC CING SYSTEM: APPLICATION UNDEREN: DATECN HORER: DATECN CONCURRENTED INTERINATION UNDERENTED INTERINATION UNDER	
ication US/090617 37 TTON: ang, xiaodong ilu, xuesong FRAGM INTION: DNA FRAGM UDENCES: E ADDRESS: E ADDRESS: Arnold, White & O. Box 4433 ton SABLE FORM: ABABLE FORM: RABLE FORM: RABLE FORM: SABLE FORM: SABLE FORM: SABLE FORM: SABLE FORM: COMPATIBLE SYSTEM: PC COMPATIBLE CATION DATA: INUMBER: US/09/0 ICONCULTENTLY	630 3 630 4 870 4 870 4 870 4 870 4 871 8 871 8 8 871 8 871
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RESULT 3
US-09-610-401-3
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; ORGANISM: Mus
US-09-610-401-4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/610,401
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: JP 11-193235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHIBATA, Takehiko
TITLE OF INVENTION: Antibody against cleavage product of vimentin
FILE REFERENCE: 522.1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MORISHIMA, APPLICANT: NAKANISHI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
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                                                                                     IKTVETRDGQVIN 456
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                                                                                                                                                                                                          QGPFDMDSCLSRHSINPYSNRESRI----LFSTWNLDHI---
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Keiko,
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                                                                              ; SEQ ID NO 18
; LENGTH: 219
; TYPE: PRT
; ORGANISM: MUS N
US-09-069-023-18
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US-09-069-023-18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-610-401-3
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
Query Match 5...
Best Local Similarity 25.1
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4%; Score 97; DB 4; Length 466 Best Local Similarity 20.8%; Pred. No. 0.088; Matches 65; Conservative 46; Mismatches 112; Indels
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                                                                                                                                                                                                                                                               APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 11-193235
PRIOR FILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: DATE: 1999-07-07
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APPLICANT:
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TITLE OF INVENTION: Antibody against cleavage product of vimentin
FILE REFERENCE: 522.1004
CURRENT APPLICATION NUMBER: US/09/610,401
CURRENT FILING DATE: 2000-07-05
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
                                                                                                                                                                                   SOFTWARE: Patentin
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 38
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                                                                                                    musculus
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5.1%; Score 91; DB
25.8%; Pred. No. 0.1;
Live 21; Mismatches
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                                        BB
                                        4.
                                      Length 219;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (512)474-7577
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPPRATING SYSTEM: PC-DOS/MS-DOS
COPPRABLE: DRIVER BY DRIVERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MCMILLIAN, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNBER: US/09/061,702 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wh.
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN ITLE OF INVENTION: APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                  oca1
173 SYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFD- 231
                                                                                                     113 PQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIRSYLREVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 CDFQGVGPKRVLRELLRGTSSQL------QGLGHMLLGISSTLRHVVEGADR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 EQGQSWSPKSGMLSYGLGREKPKHSKDIARITFDVYKQNPRDLFGSLNVKATFYGLYSMS 162
                                                             117 DSGAGL-----KWKNVARELK------EDLSSIILLSEEDLQMLVDAPCSDLAQELR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 CDEQAPORORLLADILHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRIR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4, Application US/09061702
5. 6165737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 RSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVPDNAELVLL 72 | : | : | : | : | : | : | : |
                                                                                                                                                69 IVDDDDYFLCLPSNTKFVALASNEKW------
                                                                                                                                                                                    54 EL-TEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQA 112
                                                                                                                                                                                                                            10 PESGEIRTLKPCLLRRNYSREQHGVAA-SCLEDLRSKACDILAIDKSLTPVTLVLAEDGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 TLGQAW---QGYVS------DIRRFLSAFHEPQ-----VGLIQAAQQLL 107
                                                                                                                                                                                                                                                                  5 PKSVKLRALR-----SPRKFGVAGRSCQEVLR-KGC--LRFQLPERGSRLCLYEDGT 53
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X
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                                                                                                                                                                                                                                                                                                            Conservative 49; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xuesong
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                                                                                                                                                                                                                                                                                                                           5.0%; Score 89; DB 4; Length 331; 22.2%; Pred. No. 0.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UTSD: 546
                                                                                                                                              ----AYNNSDGGTAWISQESFDVDET 116
                                                                                                                                                                                                                                                                                                            78;
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                 Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer APPLICANT: Shah, Purt TITLE OF INVENTION: NOVEL NETITLE OF INVENTION: PROTEIN NUMBER OF SECURNCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
BPLICATION NUMBER: US/08/847,900
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 442368
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LENGTH: 457 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                                                                                                                                                                                               Local
288 YFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQPVRKRQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 EVDAVDTGMSRET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 ----MDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 QSCATV-QRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQE---ESKAAFGE 218
                                                                                                   101 QAAQQLLCDEQAPQRQ-RLLADLLHNVSQNIAAETR--AEDPPWFE------GLESRF- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 ----LSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQ 299
                                                                                                                                                                   44 SRICLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQ---VGLI 100
                                                             50 VAPQQTMCSRDARTKQLRQLLEKVQNMSQSIEVLDRRTQRDLQYVEKMENQMKGLESKFR 109
                                                                                                                                                                                                                            60;
                                                                                                                                         9 SLLVLLVMGTELTQ----VLPTNPE-----ESWQVY-----SSAQDSEGRCICTV 49
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                         5.0%; Score 89; DB 2; Length 457; llarity 21.8%; Pred. No. 0.62; Conservative 40; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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PER: 36,749
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                                                                                                                                                                                                                       71; Indels 104;
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Larson, Marina

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLO,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US
FILING DATE: 03-31-1989
ID NO:4:
                                                                                                                 COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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APPLICANT:
                                                             CURRENT APPLICATION DATA:
                                                               COMPUTER: LDD COMPUTER: MS DO COMPUTER: MS DO COMPUTER: WORD DATA:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
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                                                                                                                                                                                              ADULE
STREET: ...
STREET: ...
                                                                                                                                                                                                                                                                                                ITLE OF INVENTION:
                              APPLICATION NUMBER: FILING DATE:
               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 PRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAE----LVL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                                PO Box
                                                                                                                                                                                                                                                                                                                                                                Huq, A.H.M. Mahbubul
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                                                                                                                                                                                                                                                                                                                                                                                              Hayden. Michael R.
                                                                                                                                                                                                                                                                                                                                              Chopra, Vikramjit Singh
                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                               Kalchman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                Huntington's Disease
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                                                                                              MS DOS 5.0
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                                                                                                                                                                                                                                                                                                                                 Michael
                                              US/09/085,199B
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Pred. No. 1:
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                                                                          US-09-069-023-32
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US-09-069-023-32
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                                                                                         SEQ ID NO 32
LENGTH: 331
TYPE: PRT
ORGANISM: Mus musculus
   Query Match 4.9%; Score 87; DB 4; Length 331; Best Local Similarity 22.4%; Pred. No. 0.62; Matches 81; Conservative 50; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
                                                                                                                                                              SOFTWARE: PatentIn Ver.
                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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HYPOTHETICAL: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    Application US/09069023A
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Pred. No.
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     18;
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CLASSIFICATION: 424 PRIOR APPLICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 91201398.4 FILING DATE: 06-JUN-1991 PRIOR APPLICATION NUMBER: EP 92200781.0 FILING DATE: 18-MAR-1992 PRIOR APPLICATION NUMBER: P92200781.0 FILING DATE: 18-MAR-1992 PRIOR APPLICATION NUMBER: PCT/NL92/00096 FILING DATE: 05-JUN-1992 ATTORNEY/AGENT INFORMATION: NAME: MOTAN; Thomas: F REGISTRATION NUMBER: 10,579 REFERENCE/DOCKET NUMBER: 44819 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9550	orman, I ulenberg TTION: TTION: TTION: ENCES: ENCES: Copper ork Rockefel Ork York A BLE FORM Elopp BM PC OSTEM: I TENEN ATION DA ATION DA ATION DA	Qy 337 RO 338 Qy 37 RO 338 Db 298 QQ 299 RESULT 10 US-08-157-005-3 ; Sequence 3, Application US/08157005 ; Patent No. 5620691 ; GENERAL INFORMATION: Wenswoort, Gert ; APPLICANT: Wenswoort, Gert	Db 169 QRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQE 210 222 GWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAI 276	5 PKSYKLRALRSPRKFGVAGRSCQEVLR-KGGLRFQLPERGSRLCLYEDGT
ארגעע פטע טע טע		Db 671LFHSHFHQHCXVTLSCĞHHAĞSKECSQCQSPVGAGRSPLDAVİKQIPYK 719 Qy 243 PYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYEYGLLF 294	OY 100 IOAAQOLLCDEQAPQRORLADILHNUSQNIAAETRAEDPPWFEGI 145	TELEFAX TELEX: INFORMATION SEQUENCE LENGTH: TYPE: TYPE: MOLECULE MOLECULE LOGINE MOLECULE LOGINE MOLECULE OB-157-005- Query Match Best Local S Matches 63

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RESULT 12
US-09-565-864-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (801) 531-916 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 22.18;
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                                                                                ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                   CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wensvoort,
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              TITLE OF
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                APPLICATION NUMBER: US/09/565,864 FILING DATE: 05-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                CITY: New York
STATE: New York
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                                                                                                                                                                                               COUNTRY: USA
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INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
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               <Unknown>
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Pred. No. 6.8;
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                                                ; ORGANISM: Homo US-09-069-023-12
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                                                                                                                      SEQ ID NO 12
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Best Local S
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                                                                                  LENGTH: 2:
TYPE: PRT
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-565-864-3
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  Query Match
Best Local Similarity
                                                                                                                                                                                            APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILLE OF INVENTION: SIGNALING PATHWAY INHIBITORS.
FILLE REFERENCE: UN-0333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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TELEPHONE: (212) 977-9550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 IQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAETRA------EDPPWFEGL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 315-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Moran,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: E
FILING DATE: 06-JUN-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09069023A
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ilarity 22.18;
Conservative 41
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4.8%;
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Pred. No. 6.8;
41; Mismatches
  Score
Pred.
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    NO ;
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    DB 4;
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                      Length 219;
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RESULT 14
US-08-286-819A-27
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                                                                            TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1/--
STREET: 1/--
STREET: Virginia
TRATE: Virginia
TR.A.
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                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/:
APPLICATION NUMBER: PCT/:
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                           SEQUENCE CHARACTERISTICS LENGTH: 2296 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 10-AU CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 31-OC
                                                                                                                                                                                                                                 LASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 TLGQAW 78
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                       amino acid
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                                             2296 amino acids
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                                                                                                                                                                                                                       31-OCT-1990
N: 435
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10-AUG-1992
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                                                                                                                                                                                                                                                                                                                  PCT/FR/91/00855
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                                                                                                                                                              660-060-0 PCT
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Best Local Similarity
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-AUG-
PRIOR APPLICATION DATA:
                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1755 S.
CITY: Arlington
STATE: Virginia
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                                                                                  REFERENCE/DOCKET NUMBER:
                                               TELEPHONE:
                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                 (703) 413-3000
                                                                                                                                                       JMBER: FR 9013579
31-OCT-1990
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                                                                                                                 6013508man F.
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                                                                                              24,618
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION UNBER: US 08/174,682
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 amino aci
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1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/917,146
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; TOPOLOGY: linear
; MOLECULE TYPE: protein.
US-08-980-357-27
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Best Local Similarity
Matches 33; Conserv
                                                                  Matches
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Best Local
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                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9422083.7 FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/GB95/02561 FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,955
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                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LRYSCES-RIRSYLREVSSYPSTYGAEAQEEFLRYLGSMCQRLRSMQY----NGSY----
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                            SGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAK 212
                                                                                                                                                                            amino acid
 SAYLCMSCDAQVHSANRVAS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Nixon & Vanderhye PC
8th Floor, 1100 No. 6077994th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coupland, George M.
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                                                                             4.78;
22.68;
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Pred. No. 17;
[7; Mismatches
                                                                            Score 84.5;
Pred. No. 1.
                                                             ed. No. 1.4;
Mismatches
-RHKRVRVCES-CERAPA-
                                                                                         DB 3;
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                                                               64;
                                                                                            Length 373;
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                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                             71;
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                                                          Gaps
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71
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; SOFTWARE: PatentIn Ver. ; SEQ ID NO 31; LENGTH: 239; TYPE: PRT; ORGANISM: Mus musculus US-09-069-023-31
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Best Local S
Matches 24
Best Local Similarity
Matches 23; Conserva
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Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 16
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Mus (
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                       APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TLGQAW 78
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                                                                                                                                                                                                                                                                                                                             Nunez, Gabriel
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 Conservative
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                    4.7%; Score 83.5; DB 28.8%; Pred. No. 0.89;
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   19; Mismatches
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                                     DB 4;
   35;
                                   Length 239;
   Indels
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3 QKPKSVKLRALRSPRKF--GVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDY 59

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CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 2618
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-28
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US-09-069-023-20
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Matches 54
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Patent No. 622506
                                                                                                                                                                                                      Sequence 20, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
PPLICANT: Beyer, Stefan
PPLICANT: Bloecker, Helmut
PPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
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APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Meller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
FILE REFERENCE: PCT/US 99/23535
                  APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM.03333
FILE REFERENCE: UM.03333
CURRENT APPLICATION NUMBER: US/09/069,023A
                                                                                                                                                                                                                                                                                                                                                                     2214 LALARHLARKYRATLILAGRRGAP---ARELWHQAPAEFVPVAAAIAQMEECGAR 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2161 MGAAPGPEEIALRGTSRWELGYEPVEGGTVSTISSRLREGGVYLITGG------LGGLG 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2117 ---PEVGLLRGPVRVIPFEFPNLRLRLI-------DLDSADPIWRSGCEPLLRE 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2062 PERDSPLARLEHLTELGFHHLLALARQLEAVGAPEVRLAVVTTGLAAIGGESELR----- 2116
                                                                                                                                                                                                                                                                                                                                                                                                                          192 SMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPF------DMDSCLSR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 -----SRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 PERGSRLCLYEDGTELTEDYFPSVPDNAE-----LVLLTLGQAWQGYVSDIRRFLSA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cn 4.7%; Score 83.5; l Similarity 23.0%; Pred. No. 35; 54; Conservative 25; Mismatches
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TYPE: PRT
; ORGANIZM: Drosophila melanogaster
US-09-069-023-20
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 299
                                                                                                                                                 Query Match 4.6
Best Local Similarity 29.7
Matches 22; Conservative
72 ENTELVAVFPGEHW 85
                                  65 DNAELVLLTLGQAW 78
                                                                        12 KPFKVKDVTRNIKKAVCASSLEEIRSKVAEKFEKCDHLPTIHLDSDGTEIDDEEYFRTLD 71
                                                                                                             6 KSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTEL-TEDYFPSVP 64
                                                                                                                                                 4.6%; Score 82.5; DB 4; Length 299; 29.7%; Pred. No. 1.6; ative 16; Mismatches 35; Indels
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Gaps

Search completed: May 26, 2003, 15:24:23 Job time: 23 secs

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OM protein - protein search, using sw model

Run on: May 26, 2003, 15:14:07; Search time 37 Seconds (without alignments) 878.201 Million cell updates/sec

Title: US-09-748-451-2
Perfect score: 1789
Sequence: 1 MLOKPKSYKLRALRSPRKFG.....SRIYKPQTRLKRKOPYRKRQ 338

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25 27 28 29	118 22 23 24	11 12 14 15 16	55 A A D S S S S S S S S S S S S S S S S S	Result No.
89.5 89.5 89.5 89.5	91.5 91.5 91.5 91 91	96.5 93.5 92.5 92.5	99.5 99.5 98.5 98.5 98.5	Score 108.5 105.5
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888888		2221222	2122222	222
173719 173719 173636 173636 1728896 A43554	A72096 E81573 E86527 A29329 C87555 B84497	148771 AG3174 C38888 C3176 C38888 GNLJG5 S54784 A29176	I46569 A25074 A43803 AF0627 I48128 VEHY S222119	ID A53188 T02213 JT0382
glucose-6-phosphat calo protein - fru neuronal olfactome hypothetical prote desmin - African c	ct34 hypothetical conserved hypothet CT34 hypothetical vinentin - chicken hypothetical prote hypothetical prote probable astionate	mouse tate syn on 10 pr tropepsited protected		Description pericentrin - mous NBS-LRR type resis apolipoprotein B -

A; Residues: 1-571 <LEI>

45 85.5	44 85.5	43 86	42 86	41 86		39 86				35 87	. 34 87.5	33 87.5	32 88.5		30 88.5
4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9	4.9	4.9	4.9	4.9
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C4HU	T51360	H85362	T14155	S37711	B43549	A43549	C75632	138127	T41099	T45283	S78061	GNLJGG	A24558	T13592	S12153
complement C4A pre	kinesin-like heavy	hypothetical prote	zinc finger protei	kinesin heavy chai		vimentin 1 - Afric	probable hemolysin	phosphoprotein pho	staurosporine targ	growth polarity ma	DNA-directed RNA p	HIV-1 retropepsin	complement C4 prec	hypothetical prote	pol polyprotein -

ALIGNMENTS

A;Accession: T02213 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DA: A;Molecule type: DA:
A)Title: Rapid reorganization of resistance gene homologues in cereal genomes. A; Reference number: Z14623; MUID:98081880; PMID:9419382
R;Leister, D.; Kurth, J.; Laurie, D.A.; Yano, M.; Sasaki, T.; Devos, K.; Graner, A.; Proc. Natl. Acad. Sci. U.S.A. 95, 370-375, 1998
<pre>C:Species: Oryza sativa (rice) C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 17-Nov-2000 C:Accession: TD02013</pre>
T02213 NBS-LRR type resistance protein - rice (fragment)
RESULT 2
Db 317 AKELELETLQASYEDLKAQSQEE-IRLLMSQLESMKTNREELNGSW 361
AEAQEEFLRVLGSM
Db 257 LSEQKVELEKIFQAKHEAEVSLKNLEAQHQAAIKKLQEDLQSEHCQYLQDLEQKFREKEK 316
Qy 108 CDEQAPQRORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSG 154
Db 198 AAELKEKLRSEMEKNAQ-TIETLKQDWESERELCLENLRQELSLKHQSEMEGLQSQFQKE 256
QY 52 GTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLL 107
QY 2 LOKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYED 51
Ouery Match 6.1%; Score 108.5; DB 2; Length 1920; Best Local Similarity 23.9%; Pred. No. 1.7; Matches 56; Conservative 45; Mismatches 90; Indels 43; Gaps 11;
A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1920 <dox> A;Residues: 1-1920 <dox> A;Cross-references: GB:U05823; NID:g458667; PIDN:AAA17886.1; PID:g458668 C;Keywords: coiled coil</dox></dox>
 3
R;DOXSey, S.J.; Stein, P.; Evans, L.; Calarco, P.D.; Kirschner, M.
pericentrin - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999.
RESULT 1 A53188

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A;Gene: apoB
A;Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3
A;Note: the list of introns may be incomplete
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; cholesterol metabolism; LDL; 1
                                                                                                                                                                                                                                                                                                             R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, Gene 69, 213-229, 1988
A;Title: Molecular genetics of the apolopoprotein B gene in pigs in relation to A;Reference number: 146567
Eccession: 146567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apollopprotein B - pig (fragments)
c;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
C;Accession: JT0382; I46567; I46568
R;Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF032688; NID:g2792219; PIDN:AAB96985.1; PID:g2792220 C;Genetics:
A;Gene: r1
A;Gene: r1
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Molecular genetics of the apolipoprotein B gene A;Reference number: JT0382; MUID:89108006; PMID:2905687 A;Accession: JT0382
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A; Residues: 239-1778 <MA3>
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A; Residues: 1-1778 <MAE>
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                                                                                                                                                                                                                                ecule type: DNA
sidues: 1-8,'S',10-238 <MA2>
Cross references: GB:M22646; N:
Accession: 14558
   Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                         Cross-references: GB:M22647;
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                                                          ly: apolipoprotein B
atherosclerosis; cholesterol metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YGLLFTSENLKLVHIVCHKKTTHKLNCDPSRI
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                5.8%;
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20.7%;
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   52;
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Score 104; DB Pred. No. 3.8; 52; Mismatches
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C;Species: Sus scrofa domestica (domest
C;Date: 21-Feb-1997 #sequence_revision
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                             IIEKKRTIIPTLVEAI------KEQDGREVDWEYFYGLLFTSENLKLVHIVCHK---
                                                                                                                                                                                                                                                                                                                                                                         Conservative
 TMKEIISDYHQQFIYKLQDFSDQLSDYYE--KFIAETERLIDLSIQKYHM
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ATDFASQLSSQVEQFVQE----DIQEYLSILADADGKGKEKIAELSSRAQEII-KSWAV--
                                                                                                                                                                                                                                                             SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS
                                                                                                                                                                                                                                                                                                                          RSYLREVSSY-----PSTVG-----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR
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                                                                                                                                                                                            GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH
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                                                             IIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENL
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TMKEIISNYHQR----FIYKLLDFSDQL
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A; Residues: 1-2629 <PUR>
A; Cross: references: GB:L11235; NID:g164371; PIDN:AAA74655.1; J. Lipid Res. 34, 1323-1335, 1993
A;Title: Nucleotide sequence encoding the carboxyl-terminal A;Reference number: I46569; MUID:94014802; PMID:8409766
A;Accession: I46569 C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodc RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKARK ATDFASQLSSQVEQFVQE---DIQEYLSILADADGKGKEKIAQLSSRAQEII-KSWAV--GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS RSYLREVSSY------PSTVG-----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR EEELTRLKEKKLADFINDIQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEFIQNTLWEA IKFTFDSVKYQLTDVVSEYGEQLKSLSQDVQKALSDLHSINITEILSELQIFLEGIFQEI 2374 ------VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----RFQLPER-----GSRLC-------LY---EDGTELTEDYFPSVPDNAEL------DEQAPORORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI---5.6%; 18.7%; 61; (domestic pig) svision 21-Feb-1997 #text_change 13-Aug-1999 Score 99.5; Pred. No. 15; from Mismatches GB/EMBL/DDBJ B 140; 2 Length Indels half of apolipoprotein 2629; PID:g951375 113; Gaps 260 2314 2492 209 2434 108 2546 164 69

2594

A; Residues: 5-12;14-28;37-69 < AND> A; Accession: B31951	_	232 AFLANDHEEELQELQAQIQEQHYQIDVDVSKPDLTAALKDVKQQY-ESVAAKNLQEAEEW 290	Ş
A; Molecule type: protein			!!
9.6		87 RFLSAFHEPOVGLIOAAOOLLCDEOAPORORLLADILHNVSONTAAFTRAFTDDW 141	Qy
try 28, 2974-2979, 19 Domain- and sequence-		180 EDIMRLREKLQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEI- 231	Db
A;Cross-references: EMBL:X56397; NID:g5 R;Ando, S.; Tanabe, K.; Gonda, Y.; Satc		27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86	γо
s: 1-155,'I	· ·	es 65; Conservative 47; Mismatc	ма
A; Accession: S14526		5.5%; Score 99; I	D O
A: Reference number: \$14526		Keywords: coiled coil; intermediate filament; phosphoprotein	
submitted to the EMBL Data Library, Oct		keratin	C; Su
A; Cross-references: EMBL: M26251; NID: g2		A;Map position: 10p13-10p13 A:Introns: 18872: 20873: 24073: 29473: 33673: 41072: 42571: 45373	A; Ma A; In
A; MOLECULE type: mRNA A; Residues: 1-155, 'EL', 158-337, 'E', 339-		A;Cross-references: GDB:119630; OMIM:193060	A;Cr
A;Status: translation not shown			C; Ge
 ⊃		A;Residues: 167-466 <res> A;Cross-references: GB:M25246; NID:g340233; PIDN:AAA61282.1; PID:g340234</res>	A;Re
Mol. Gen. Genet. 221, 33-36, 1990 A:Title: Coding sequence and flanking r		Catus: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA	A; Mo
A; Cross-references: GB: M24849; NID: g202 R; Hennekes, H.; Kuehn, S.; Traub, P.		cession: I54056	
A; Residues: 1-155, 'EL', 158-337, 'E', 339-	from a human	Isolation of a human vimentin cDNA with a long 3'-noncoding region	
A; Accession: JS0241			R;Gu Gene
A; Title: Vimentin cDNA clones covering A; Reference number: JS0241; MUID: 893066		A;Cross-references: EMBL:X16478; NID:g37847; PIDN:CAA34499.1; PID:g37848	A;Cr
		A; Molecule type: mRNA	A; Mo
A;Cross-reierences: EMBL:Z22526; NID:gl R;Wood, L.; Theriault, N.; Vogeli, G.	-	Status: preliminary	A;St
Residue		37; MUID:89303836; PMID:2472876	A; Re
A;Status: preliminary A:Molecule type: DNA	breast cand	y keratin expression in some hormone-independent	A;Ti
A; Accession: S32832	Clark, R.	S.E.; Worland, I	R; So
tion: Upstream region of to ce number: S32627		9-466 <per> esidue 287 as</per>	A; Re A; No
submitted to the EMBL Data Library, Apr		P	A; Mo
Cross-ref	,	71665	A; Re
A; MOLECULE TYPE: mRNA A; Residues: 1-466 <cap></cap>	transcript	tide sequence of the human v	A;Ti
Accessi		D.	R; Pe
A; Title: Mouse vimentin: structural rel A; Reference number: A43803; MUID: 902656		A;Residues: 1-41,'D',43-441,'E',443-466 <fer> A;Cross-references: GB:M14144; NID:g340218; PIDN:AAA61279:1; PID:g340219</fer>	A; Cr
:		type: DNA	A; MO
C;Accession: A43803; S32832; JS0241; S1		Reference number: A25074; MUID:87089701; PMID:3467175 Accession: A25074	A; Re
C;Date: 12-Feb-1993 #sequence_revision		Title: Coding sequence and growth regulation of the human vimentin gene.	A;T1
מ	Riel, J.K.;	rrari, S.; Battini, R.; Kaczmarek, L.; Rittling, S.; Calabretta, B.; De Cell. Biol. 6. 3614-3620. 1986	R; Fe
A43803	•	D:g37849	4
		lecule type: mRNA	
Db 444 IKTVETRDGQVIN 456		A.Reference number: S13115; MUID:91067467; PMID:2251132	A: Re
	himan wind	coding part	Nucl A:T1
	Leffers, H.	Andersen, A.; Walbum, E.; Celis, J.E.;	R; Ho
		C;Date: 30-Jun-1988	C; Ac
Qy 227 QGPFDMDSCLSRHSINPYSNRESRI	-		C; Sp
Db 351 FAVEAANYQDTIG-RLQDEIQNMKE		5 (A25074
PSTVGAEA			BESTIT
Db 291 YKSKFADLSEAANRNNDALRQAKQE		2595 FLRYIMKLLKELQSDTVNDMRPYIKV 2620	Db
Qy 142 FEGLESRFQS		309KTTHKLNCDPSRIYKPQTRL 328	Qy
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55-337,'E',339-466 <POD>
955407; PIDN:CAA39807.1; PID:g55408
hto, C.; Inagaki, M.
c phosphorylation of vimentin induces disassembl 2884; PMID:2500966
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S12774; S14526; A31951; B31951; S32627
, K.; Starnes, S.
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9202369; PIDN:AAA40556.1; PID:g202370
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02367; PIDN:AAA40555.1; PID:g202368
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mouse vimentin gene.
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A; Molecule type: protein
A; Residues: 5-12; 14-69 < AN2>
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil; intermediate fi
F; 104-138/Region: coil 1A
F; 147-247/Region: coil 1B
F; 264-282/Region: coil 2A
F; 291-411/Region: coil 2A
F; 291-411/Region: coil 2A
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Best Local S
Matches 89
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                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:AL513382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: AF0627
                                                                                                                                                                                                                                                                                                                                                                                                                                              ference number: AB0502; Accession: AF0627
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; Moule, S.; O'Gaora, P.
; Moule, S.; O'Gaora, P.
re 413, 848-852, 2001
hors: Parry, C.; Quail, M.; Rutherford, K.; Simm le: Complete genome sequence of a multiple drug
                                                            152
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                                                                                                                                                                                      Similarity
       VLLTLGQAWQGYVSDI - - - RRFLSAFHEPQVGLI - - -
                                                    CREIWRK-CLAWLQDSEGSRQQHNQAYADAMLEAHADFFTQIESSPLNPSQARAVVNGES
                                                                                                         CQEVLRKGCLRFQLPERGSRL---CLYEDG-TELTEDYFPSVPD----
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                                                                                                                                                         Score 98.5; DB Pred. No. 3.1; 52; Mismatches
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Davis, P.; Davies, R.
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.M.; Dowd, L.;
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A;Residues: 1-448 <RES>
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     golden
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C;Species: Cricetulus griseus (Chinese C;Date: 04-Sep-1997 #sequence_revision C;Accession: 148128 R;Bloemendal, H.; Quax, W.; Quax-Jeuken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Organization and expression of the vimentin A;Reference number: I48128; MUID:83297272; PMID:66884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vimentin - Chinese hamster (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M16718; NID:g191232; PIDN:AAA37029.1; PID:g387058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
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                                             273 VEAIKEQDGREVD
                                                                                                                                                                                                                                                                                                                                                                                        214 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 5.5%;
Similarity 20.1%;
63; Conservative (
IKTVETRDGQVIN
                                                                                                 KMALDIEIATYRKLL---
                                                                                                                                              QGPFDMDSCLSRHSINPYSNRESRIL----FSTWNLDHI----
                                                                                                                                                                                              FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ-----
                                                                                                                                                                                                                                           YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC
                                                                                                                                                                                                                                                                                           YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                                                          F-----EGLESRFQSKSGYLRY----
                                                                                                                                                                                                                                                                                                                                                                                                                                       RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDIIR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLDTTYRFN---SRIGDIANRFVQQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHKKTTHKLNCDPSRIYKPQTRLKRKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFQDISPQRAALLEALRKQNSQTTLFAVGDDWQAIY--RFSGAQLSLTTAFHQTFGEGEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECRELFGKRIKLMAPLLKAWKSALKAENAVDFS--GLIHQAMVILEKGRFISPWKHILVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLEEEMQWVVPEGNFWDDETLQRRLAPRLDRWVSLMRMHG-----GAQAEMIAGAPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLREVSSYPSTYGAEAQEEFL; -- RVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWF
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, 115-118, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLVEAIKEQDGREV-----DWEYFYGLLFTSENLKLVHIV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                            EGEESRISLPLPNFSSLNLRETNLESLPLVDTHSKRTL---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98; DB:
Pred. No. 2;
47; Mismatches
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                                                                                                                                                                                              ----DLLNV
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RESULT 10
$22119
vimentin - rat
c;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
C;Accession: $22119; JQ1389
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C;Date: 19:Feb-1984 #sequence_revision 27-Nov-1985 #text_change 22-Jun-1999
C;Accession: A90842; A93953; A39731; A02959
R;Quax, W.; Egberts, W.V.; Hendriks, W.; Quax-Jeuken, Y.; Bloemendal, H.
Cell 35, 215-223, 1983
A;Title: The structure of the vimentin gene.
A;Reference number: A90842; MUID:84026520; PMID:6194898
A;Accession: A90842
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A; Residues: 36-41'A', 42-47', 'T', 48:49,50-62:63-67 <CHO>
A; Residues: 36-41'A', 42-47', 'T', 48:49,50-62:63-67 <CHO>
A; Note: the phosphorylated residue described as 40-Ser may be 41-Ser;
C; Comment: The initiator Met is not shown.
C; Comment: Vimentin occurs in intermediate-sized filaments in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aperimental source: lens
R;Chou, Y.H.; Ngai, K.L.; Goldman, R.
J. Biol. Chem. 266, 7325-7328, 1991
A;Title: The regulation of intermediate filament reorganization in mitosis. p34(cdc2) pt
A;Reference number: A39731; MUID:91210232; PMID:2019567
A;Accession: A39731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GB:K00927; NID:g191465; PIDN:AAA37104.1; PID:g387077; Ouax-7euken, Y.E.F.M.; Quax, W.J.; Bloemendal, H. roc. Natl. Acad. Sci. U.S.A. 80, 3548-3552, 1983; Pitle: Primary and secondary structure of hamster vimentin predicted from the nucleotic Reference number: A93953; MUID:83221633; PMID:6304716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1/Modified site: acetylated amino end (Ser) *status predicted 41/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) *status predicted 52,64/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: cytoskeletal keratin Keywords: acetylated amino end; coiled coil; intermediate filament; phosphoprotein 461/-64/Domain: tail <TLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment: The initiator Met is not shown.
Comment: Vimentin occurs in intermediate-sized filaments in various nonepithelial cel
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Residues: 1-464 <QUI>
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cession: A93953
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|coule type: mRNA
|sidues: 'PRHLEPAG',25-40,'A',42-113,'D',115-180,'T',182-464 <QU2>
                                                                                                                                                                                                                                                                                      273 VEAIKEODGREVD 285
                                                                                                                                                                                                                                                                                                                                                  388 KMALDIEIATYRKLL----EGEESRISLPLPNFSSLNLRETNLESLPLVDTHSKRTL----L
                                                                                                                                                                                                                                                                                                                                                                                                    227 QGPFDMDSCLSRHSINPYSNRESRIL-----FSTWNLDHI------IEKKRTIIPTL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 EDIMR----LREKLQEE-----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 QEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity 20.1%;
                                                                                                                                                                                                                                   IKTVETRDGQVIN 454
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Pred. No.
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RESULT 11
[148771] - mouse (fragment)
Slp(w7) - mouse (fragment)
C.Speciles: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C.Accession: I48771
                                                                                                                                                                                                                                                                                                                                          R;Hemenway, C.; Kalff, M.; Stavenhagen, J.; Walthall, D.; Robins, D. Nucleic Acids Res. 14, 2539-254, 1986
A;Title: Sequence comparison of alleles of the fourth component of complement A;Reference number: I48274; MUID:86176748; PMID:3008092
A;Accession: I48771
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A;Experimental source: prostatic tumor; cell line Dunning R-3327; Strain Fische R;Bussemakers, M.J.G.; Verhaegh, G.W.C.T.; van Bokhoven, A.; Debruyne, F.M.J.; Biochem. Biophys. Res. Commun. 182, 1254-1259, 1992
A;Title: Differential expression of vimentin in rat prostatic tumors.
A;Reference number: JQ1389; MUID:92171936; PMID:1540169
A;Accession: JQ1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bussemakers, M.J.G.; Verhaegh, G.C.W.; van Broken, A.; Debruyne, F.M.J.; Schalken, submitted to the EMBL Data Library, October 1991
A;Description: differential expressions of vimentin in rat prostatic tumors: complete A;Reference number: S22119
A;Accession: S22119
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A; Residues: 1-466 <BUW>
                                                                                                                                                                                                 C; Superfamily: alpha-2-macroglobulin
                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-594 <RES>
A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X62953
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A; Residues: 1-466 <BUS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 FALEAANYQDTIG-RLQDEIQNMKEEMARHLREYQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 EDIMR----LREKLQEE----MLQREEAESTLQSFRQDVDNASLARLDLERKVESLQEEI- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 VEAIKEQDGREVD 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 YLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 YKSKFADLSEAANRNNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMREMEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 AFLKKLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQY-ESVAAKNLQEAEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 RFLSAFHEPQVGLIQAA-----QQLLCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
18 KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY----EDGTELTEDYFPSVPDNAEL
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                                                                                      Similarity
58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                      Conservative
                                                                                                                                                                                                                            EMBL: X06454; NID: g54105; PIDN: CAA29760.1; PID: g54106
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Pred. No.
                                                                                                                                        Score 98;
                                                                                                                 Pred.
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                                                                                                                 No.
                                                                                                                                            DB 2; Length 594
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                                                                                82;
                                                                                      Indels
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.M.J.; Schalk
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C; Accession: AG3174
R; Wood, D.W.; Setubal, J.C.; Kaul, R.;
erage, G; Gillet, W.; Grant, C.; Guent
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A; Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294, 2317-2; A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GB:AE008687; PIDN:AAL45813.1; ;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome: plasmid
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Nate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Similarity 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       LASIVGPKSL---GRHTVEIVREADLVVLIGTRIN----QNGTDNWRQYSP----DAQI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G 540
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         VRKRQ 338
                                                                                                                                                                                                                                                                                                         QNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCES-----RIRSYLREVSSYPSTVGAE 181
                                                                                                                                                                                                                                                                                                                                                 IHIDTDPQEVGRNFEAIRLVGDARETLAGL-----
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                                             ILGFQRDAETVKFGKYTTACHFAE:
                                                                                ----EQDGREVDWEYFYGLLFTSENLKLVHIVCHKKTTHKLNCDPSRIYKPQTRLKRKQP 333
                                                                                                                       DGGFA----
                                                                                                                                                        -GWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTW-NLDHIIEKKRTIIPTLVEAIK--
                                                                                                                                                                                              ASYSSMWVLGQLRISSERTRVLT-----PRGLAGLGWGVPLAIGAKVAAPESDVVALVG
                                                                                                                                                                                                                                   AQEEFLRVLGSM---CQRLRSMQYNGSYFDRGAKG------GSRLCTPE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.5; D
Pred. No. 3.6;
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                                                                                                                     -WAELETLY---RMQIPITIIVLNNG
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C;Superfamily: pol polyprotein
C;Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase;
F;106-204/Product: retropepsin *status predicted <RTP>
F;130/Active site: Asp (shared with dimeric partner) *status predict
                                                                                                                 A;Cross-references: EMBL:M19499
C;Comment: Specific enzymatic c
                                                                                                                                                                                          R; Franchini, G.; Gurgo, C.; Guo, Nature 328, 539-543, 1987
A; Title: Sequence of simian immun A; Reference number: A28873; MUID A; Accession: B28873
                                                                                                                                                                                                                                                                                                    HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green N;Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed C;Species: simian immunodeficiency virus, SIV C;Date: 30-Jun-1989 *sequence_revision 30-Jun-1989 *text_change 03-Jun-2002
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Aug-2001
C;Accession: C38888
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                                                                              A; Gene:
                                                                                                   C; Genetics:
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F; 157-380/Domain:
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C;Superfamily: Podospora anserina mitochondrion
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A; Residues: 1-397 < CUM>
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                                                                                                                                                                      A; Molecule type:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 FALLQYSIRLEKGYFLMKNLKYSTLASDYSENSLANTRNKNNSPFKEKEDRFNEWLAGII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 QAAQQL---LCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 KILVIMDNPQITKARSENYKPGITEFLGLCM-----WVGISEAIRLLPTSLSKKIKDLI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 RLCLYEDGTELT----EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLI 100
                                                                                                                                                        1-1054 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.J.; Michel, F.; McNally, K.L.
16, 381–406, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                        B28873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SKSGYLRYSCESRIRS----YLREVSSYPSTVGAEAQEEFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGDGCFQVSKKGYASLEIVTQLRDKRILYLIK-QKYGGAVKLHAGDNYLRYRLHHKAGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLINGINGLIRNPIRILQLGKICNLYDIKLKDTQPLTYYNGWLS--GFFDTDGSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein - Podospora anserina mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --YLNEKSGQIFITAS-----QKNRFILDALVELYGGTIYAMVKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPYSNRESRILFSTWNLDHIIEKKRTIIPTLVE-----AIKEQD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VLGSMCQRLRSMQYNG--SYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKKRK
                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:X55026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%;
                                                                                                                                                                                                             immunodeficiency virus and MUID:87287229; PMID:3497350
                                                                                                                 cleavages may yield mature proteins including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:M30937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                    H.G.; Gallo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:M61734; NID:g14030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kilobase pair
PMID:2558809
                                                                                                                                                                                                                                                                    R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <C19>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112;
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                                                                                                                                                                                                                               its relationship to
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   predicted
                                                                                                                                                                                                                                                                    [T]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA38788.1;
                                                                                                                                                                                                                                                                  Fargnoli,
                                         polyprotein;
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                                                                                                                                                                                                                                                                  K.A.;
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sex-limited protein Slp(w7) - mouse C;Species: Mus musculus (house mouse) C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999 C;Accession: S4784; 148770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: alpha-2-macroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 22/2; 86/3; 154/1; 177/3; 207/2; 235/1; 267/2; 302/3; 347/1; 385/3; 444/3; 5(3); 1219/1; 1296/3; 1352/3; 1372/3; 1404/1; 1464/2; 1494/3; 1519/3; 1554/1; 1584/1; 1617,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The murine Slp gene. Additional evidence that a Reference number: S54784; MUID:92013090; PMID:1918990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lecule type: mRNA
hidues: 634-641,'L',643-828 <RES>
oss-references: EMBL:X06455; NID:g54102; PIDN:CAA29761.1; PID:g899336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POCAT
                                                                                                           1570 LATL---CSGDVCQCAEGKCPRLLRSLERRVEDKDGYRMRFAC----
                                                                                                                                                                                                                                      1527 V-----GF-----GASQEVVVGLVQPASAVLYDYYSPDHKCSVFYAAPTKSQL 1569
                                                                                                                                                                                                                                                                                                                                                                        1468 KLGLSGMAIADITLLSGFHALRADLEKLTSLSDRYVSHFETDGPHVLL-YFDSVPTTREC 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                        119 LADLIHNVSQNIAAETRAEDPPWFEGLESRFQSKSGY-LRYSCESRIRSYLREVSSYPST 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 QLKELLNSIGFSTPEEKFQKDPPFQWMGYELWPTKWKLQKIELPQRETWTVNDIQKLVGV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 YIYKVLPQGWKGSPAIFQYTMRHVLEPFRKANPDVTLVQYMDDILIASDRTDLEHDRVVL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 CYYQEG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 LRYSCE-----SRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 IRIPHPAGLAKRKRITVLDIGDAYFSIP-----LDEEFRQYTAFTLPSV-NNAEPGKR 347
                                                                                                                                                                                                                                                                                                       70 VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD-----EQAPQRQRL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                         18 KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY-----EDGTELTEDYFPSVPDNAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 LVLLTLGQAWQG----YVSDIRRFLSAFHE--PQVGLIQAAQQLL--CDEQAPQRQRL-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LRSPRKFGVAGRSCOEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAE---- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYFDRG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNWAAQIYPGIKTKHLCRLIRGKMTLTEAVQWTEMAEAEYEENNI-----ILSQEQEG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2756-2763, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                      5.1%; Score ...
27.6%; Pred. No. 38;.
rative 20; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 92.5; DB 1; Length 1054; 22.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Additional evidence that sex-limited protein has no biolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 2; Length 1735; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Indels
                                                                                                           ---YYHQV-EYGFT 1619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (C4) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ogata, R.T.; Sepich, D.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984
A;Fithe: Genes for murine fourth complement component (C4) and sex-limited protein (S4);A;Reference number: A41195; MUID:84272739; PMID:6589636
A;Accession: A41195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1096-119 <0G3>
A;Cross-references: GB:X55495
R;Nonaka, M; Kimura, H.; Yeul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
R;Nonaka, K.; Simura, H.; Yeul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986
A;Title: Identification of the 5'.flanking regulatory region responsible for the diff
A;Reference number: I59084; MUID:87017050; pMID:3464002
A;Accession: I79467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1345-1438,'R',1440-1544 <OG2>
A;Cross-references: GB:K02293; NID:g199611; PIDN:AAA39682.1; PID:g199612
A;Cross-references: GB:K02293; NID:g199611; PIDN:AAA39682.1; PID:g199612
A;Toss-reference Levi-Strauss, M.; Duponchel, C.; Meo, T.
Philos. Trans. R. Soc. Lond. 306, 389-394, 1984
A;Title: Sequence heterogeneity of murine complementary DNA clones related to A;Reference number: A93753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Ogata, R.T.; Sepich, D.S.
J. Immunol 135, 4239-4244, 1985
A;Title: Murine sex-limited protein: complete cDNA sequence and comparison with murin A;Reference number: A29176; MUID:86060918; PMID:3840826
A;Accession: A29176
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                                                                                                                                                                                                                                                                                                                          C;Superfamily: alpha-2-macroglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1736/Product: sex-limited protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Ogata, R.T.; Zepf, N.E.

Eur. J. Immunol. 20, 1607-1610, 1990

A:Tittle: C4 from C4-high and C4-low mouse strains have identical sequences in A:Reference number: A60227; MUID:90353398; PMID:2387317

A:Accession: B60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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A;Title: Isolation of cDNA clones specifying the fourth component of mouse complement A;Reference number: A94013; MUID:85038607; PMID:6208559
A;Accession: B21692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: complement component C4-related sex-limited protein C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999 C;Accession: A29176; B21692; A41195; B29059; B60227; I79467
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A; Residues: 1-21 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1255-1335, 'G', 1337-1373 <TOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 651-749, 'H', 751-774, 'D', 776-802, 921-1040 < NON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex-limited protein precursor - N; Alternate names: complement co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M14226; NID:g199615; PIDN:AAA39684.1; PID:g554239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                Local
50;
                                                                     1468 KLGLSGMAIADITLLSGFHALRADLEKLTSLSDRYVSHFETDGPHVLL-YFDSVPTTREC 1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                  18 KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY----EDGTELTEDYFPSVPDNAEL 69
70 VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD-----EQAPQRQRL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B29059
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                   5.1%; Score 92; DE larity 27.6%; Pred. No. 38; Conservative 20; Mismatches
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R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, Wature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206806; PMID:10192388
A;Accession: A72096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
D70441
                                                          C >
                                                                                           A; Experimental source: strain C; Genetics:
                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-925 <ARN>
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                                                                                                                              A;Cross-references: GB:AE001614; GB:AE001363; NID:g4376562; PIDN:AAD18442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xido/reductase iron sulfur protein - Aquifex aeolicus
;Species: Aquifex aeolicus
;Spate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
                                                        Superfamily:
                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                   hypothetical protein - Chlamydophila pneumoniae (strain CWL029) ecies: Chlamydophila pneumoniae, Chlamydia pneumoniae potentia: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Ju-Accession: A72096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA Residues: 1-395 <AQF>
   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: D70441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          le: The complete genome of the hyperthermophilic bacterium erence number: A70300; MUID:98196666; PMID:9537320
 Local Similarity
                                                                             CPn0293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.; Warren, P.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         K 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DWKVFSFTEIIANEDIEFKGKGEKVTVHVPCHYYTAMKLN--PNNFYKALGKVKNAETV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKDIKCCGAPHLY -- HGNTEAFEKLKEHNLKE-IEKYEYDALVVACPTCGGALKEDYGK-
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                                                        Chlamydia
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                                                      trachomatis hypothetical protein CT234
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 5.1%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ferredoxin 2[4Fe-4S]-related proteins; ferredoxin
2[4Fe-4S] homology <FER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.5; DB
Pred. No. 5.9;
19; Mismatches
 Score 91.5;
Pred. No. 1
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   18;
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                   DB 2;
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                 Length 925;
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                                                                                                                              PID:g437656
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein CP0465 [imported] - Chlamyc C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #text_c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-925 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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77; Conserv
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                                                                                                                                                                                    HTSVRANHKPYCPELLKRLRQCSHNDEASQYLLKTISIALDISFVKDLLMTTSQLKNTSR
                                                                                                                                                                                                                                                                                                 YVSDI--RRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLLHNVSQNIAAET----
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EQDGREVDWEY-FYGLL
                                                                                                            KYAEAMIGELDKEVAPAFLQVL-
                                                                                                                                                                                                                       ----RAEDPPWFEGLESRFQ-----SKSGYLRYSCE-----SRIRSYLREVSSYPST--
                                                                                                                                                                                                                                                                                                                                        ELLKRWTSIFPHPAIASAIHLYFAEHDLLHITHIAEDLYDTVGDRLLAAILTVRRQEAYG
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                                                                      WFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPT-----LVEAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPT-----LVEAIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                               -VGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSR-----LCTPEG
                                    ---LKKHAYKIVKSKASKALFYSYH-GHYIQKK---YPTYNLSLLANTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LKKHAYKIVKSKASKALFYSYH-GHYIQKK---YPTYNLSLLANTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 91.5;
21.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                44;
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FTSENLKLVHIVCHKKTTHKLNCD
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                                                                                                            -TDEGTHNRCRILAAKALCKIDN
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A;Gene: CPj0293
C;Superfamily: Chlamydia trachomatis hypothetical protein CT234
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E86527
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lecule type: DNA
sidues: 1-925 <STO>
sidues: 1-925 (STO>
foss-references: GB.BA000008; NID:g8978667; PIDN:BAA98503.1; GSPDB:GN00142
foss-references: GB.BA000008; NID:g8978667; PIDN:BAA98503.1; GSPDB:GN00142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 SNYYAEVNEMLSLIGILGSMEHSGVLIRALTSKNQR---IKAQALESLEKNCD 831
782 SNYYAEVNFMLSLLGILGSMEHSGYLIRALTSKNOK---IKAQALESLEKNCD 831
                                                                                                                        737 WL------LKKHAYKIVKSKASKALFYSYH-GHYIQKK---YPTYNLSLLANTLN 781
                                                                                                                                                                                                                                       693 KYAEAMIGELDKEVAPAFLQVL------TDEGTHNRCRILAAKALCKIDN 736
                                                                                                                                                                                                                                                                                              178 -----VGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSR-----LCTPEG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 EQDGREVDWEY-FYGLL------FTSENLKLVHIVCHKKTTHKLNCD 317
                                                                                                                                                                            223 WFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDHIIEKKRTIIPT-----LVEAIK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 EVLRKGCLRPQLPERGSRLCLY--EDG----TELTEDYFPSVPDNAELVLLTL-GQAWQG 80
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Search completed: May 26, 2003, 15:23:48 Job time: 40 secs

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1789
1 MLQKPKSVKLRALRSPRKEG.....SRIYKPQTRLKRKQPVRKRQ 338
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O29433 sus scrofa
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O60819 homo sapien
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Q9xyd1 drosophila	096958 drosophila	Q61372 mus musculu	chi	Q88135 chimpanzee	Q95qa8 caenorhabdi	Q8un03 chimpanzee	Q9whz0 human immun	Q96wt6 schizosacch	0	Q04097 chimpanzee	_	_			Q9vwb9 drosophila	٠		Q9z8p5 chlamydia p			067558 aquifex aeo				-	Q8r5n0 mus musculu	mus	agro

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66 NAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLLHN 125	6 KSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPD 65 : : : :	Query Match 58.3%; Score 1043; DB 13; Length 333; Best Local Similarity 60.1%; Pred. No. 7.8e-86; Matches 197; Conservative 51; Mismatches 74; Indels 6; Gaps 2;	SMART; SM00266; CAD; 1. SEQUENCE 333 AA; 38474 MW; 9B069CD287755E11 CRC64;	InterPro; IPR003508; CAD.	HIGI. CIEII. 270:43427 *5452(2001). EMBL; AF406761; AAL37716.1; *.	Cleavage and Stage I Chromatin Condensation in Apoptosis.";	"CAD/DFF40 Nuclease Is Dispensable for High Molecular Weight DNA	מ	SEQUENCE FROM N.A.	\CB1_':ax1D=9031;	Gallus	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Gallus gallus (Chicken). Rukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	CAD		(TrEMBLrel. 21,	01-MAR-2002 (TEMBLEEL 20, Last sequence update)	A STANDING TO TO	Q8UVS5 PRELIMINARY; PRT; 333 AA.	, F	3

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Submitted (SEP-2001) to the EMBL/GenBank/
EMBL; AF286179; AAF99706.1; -
EMBL; AF426316; AAL40264.1; -
HSSP; O00273; ILBX.
InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
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HIVCHKKTTHKLNCDPSRIYKPQTRLKR
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                                                                                                                              PYSNRESRILFSTWNLDHIIEKKRTIIPTLVEAIKEQDGREVDWEYFYGLLFTSENLKLV
                                                                                                                                                                                                                      KSEYKKVAEALAEKLKAARYNGTYFDRSEKDANRLCTEEGWFSCQGAFDENSCNFLHSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDNTDLVLLPHGQSWNGFADEINRVLGLDRNTEELLVSAAQGLLSDERSPKRRRILGDLL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCDEQAPQRQRLLADLL 123
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                                                                                              PYGNRESRILFSTWNLDHLIEKKRTVIPALAKALEANKSNDINVDYFYKLLFTRENLKLV
                                                                                                                                                                                                                                                                                                                                             SNIRDRSELENRIODHDWFEGIDTRFKTKSAYMKYNCESRIRGYLKEVDGYTQTIKNAKT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 941;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7E15D76F8824F0FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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1.2e-76;
hes 88;
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Matches 80
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Matches 80
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01-DEC-2001
01-DEC-2001
01-MAR-2002
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Q96P74;
                                                                                                                                                                                                                                                                                                                SEQUENCE
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01-DEC-2001
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Pfam; PF02017; CIDE-N; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Payascas J.R., Yuste V.J., Perera R., Comella "Characterization of splice variants of human that show CIDE-N structure and function."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AF409962; AALO207.1; -. IPR003508; CAD. Pfam; PF02017; CIDE-N; 1.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA fragmentation
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                             DEC-2001 (TrEMBLrel. )
MAR-2002 (TrEMBLrel. )
fragmentation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
 PSVPDNAELVLLTLGQAWQG
                                             MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVPDNAELVLLTLGQAWQG
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                            MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF
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1 (TrEMBLrel. 19, 1
2 (TrEMBLrel. 20, 1
1 ntation factor B ti
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(TrEMBLrel.)
                                                                                     Conservative
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Primates;
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Primates;
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                                                                                                 23.4%;
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20,
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                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                             , Last sequence update), Last annotation updat truncated form I.
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Last annotation update)
truncated form III.
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                  Score 419; DB 4; ]
Pred. No. 3.3e-30;
0; Mismatches 0;
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Pred. No. 2.1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                              34E72888A0F3B909 CRC64;
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                                                                                                                                                                                                                                              J.Х.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caspase-activated
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PSVPDNAELVLLTLGQAWQG

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RESULT 5
Q96P73
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AC Q96P
DT 01-D
DT 01-D
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DE DNA
GN DFFB
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                                                                                                                                                                                                                                                                                                           REP4 protein (CG9414 protein).
REP4 OR DCAD OR CG9414.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                     09V3H0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDLINE-20196006: PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bayascas J.R., Yuste V.J., Perera R., Comella J.X.; "Characterization of splice variants of human caspase-activated DNase that show CIDE-N structure and function."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

SUBBL; AF409061; BAL02006.1; -.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
DNA fragmentation factor B truncated form II.
                                                                                                                           Inohara N., Nunez G.;
Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V3H0
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        MEDLINE-20085845;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                     nohara N., Nunez G.;
Genes with homology to DFF/CIDEs found in Drosophila melanogaster.";
ell Death Differ. 6:823-824(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF02017; CIDE-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVPDNAELVLLTLGQAWQG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                    PubMed=10627165;
G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.4%;
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                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 419; DB 4;
; Pred. No. 3.5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Beans D.A., Butler H., Caddieu E., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Colson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T., Gu Z., Chang R., Houck J.,
RA Harris N.L., Harvey D., Helman T., Gu Z., Chang R., Liu X.,
RA Harris N.L., Howland T.J., Wel M.-H., Ibeyman C.,
RA Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mclart K., Kemington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mclart K., Kemington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mclart K., Kemington K.A., Nixon K., Nurskern D.R., Pacleb J.M.,
RA Mclart K., Kemington K.A., Nurphy L., Muzny D.M., Nelson D.L.,
RA Mclart K., Kemington K.A., Nurphy L., Weller F., Shen H.,
RA Mclart K., Kemington K.A., Nurphy L., Scheeler
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                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                  115 P--DAVITTDADFEFEKMRQQSPLLKVA-DIFYDFIEQHPEKFRRMITEYEHQKQRRVLD
                                                                                                                            281 RIPSKRLRQVIREYTKENCILDEWSTSLCSDLGDFYCQGSYSENGNSCSKQHTINPYASR
                                                                                                                                                                                                                                                                                                172 NSKTHLSLKAEHVEWFTGGEERFHSKEEAMATRAQTRVRGYY-----YKAKEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                          QAWQGYYSDIRRFLSAFHEPQYGLIQAAQQLLCD--EQAPQR-QRLLADLLHNYSQNIAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKYGIGANSLEMLIAKAKSKFPLLE--PHLYLASDGFEVSDDEYLKSLP--AQTLFIVSG
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                                       ENLILFQVWNLDHQIELCRTILPALVANVEELVSHPQTKCSIHKKQVVDISVLEYFLE-I 399
                                                                                  ESRILFSTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD----WEYFYGLL
FTSENLKLVHIVCHKK----
                                                                                                                                                                                                              TRNPLYRQNAKARQVINSVLEKFRYLLIGCDFFSMMFDRNCKQKHEFLKQHLGDEETDAG
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Pred. No. 1.
---TTHKLNCDPSRIYK 323
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Best Local
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  048981
048981;
01-JUN-1998
01-JUN-1998
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MEDLINE-20339953; PubMed-10777599;
Yokoyama H., Mukae N., Sakahira H., Okawa K., Iwamatsu A., Nac
Yokoyama H., Mukae N., Sakahira H., Okawa K., Iwamatsu A., Nac
Yokoyama H., Mukae N., Sakahira H., Okawa K., Iwamatsu A., Nac
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR00345; CyCC_heme_bind.
Pfam; PF022017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
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J. Biol. Chem. 275:12978-12986(2000).
EMBL; AB036773; BAA97120.1; -.
FlyBase; FBgn0028406; Rep4.
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01-OCT-2000
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                                                                                                                                                                                                                                        ENLILEQVWNLDHQIELCRTILPALVANVEELVSHPQTKCSIHKKQVVDISVLEYFLE-I
                                                                                                                                                                                                                                                                             ESRILESTWNLDHIIEKKRTIIPTLVEAIKE------QDGREVD---WEYFYGLL
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nilarity 26.8%;
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    (TrEMBLrel.
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Pred. No. 1.8e-20;
1; Mismatches 121;
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Best Local S
Matches 69
                                                                                                                                 09CZL3;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
11 days embryo cDNA, RIX
clone:2700062L12, full 1
                                                       Eukaryota; |
Mammalia; E
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Oryza sativa (Rice).
Oryza sativa (Rice).
Oryza sativa (Rice).
Oryza; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530;
                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                           Q9CZL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 95:370
EMBL; AF032688; AAB96985.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
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Leister D., Kurth J., Laurie D.A.,
Graner A., Schulze-Lefert P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NBS-LRR type resistance protein (Fragment). R1.
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  SEQUENCE FROM N.A.
                                  NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                           SIGRLFNLQTLKL----
                                                                                                                                                                                                                                                                                                                                                                                                  -YGLLFTSENLKLVHIVCHKKTTHKLNCDPSRI
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                                                         Eutheria;
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571 AA;
                                                                                                                             (TTEMBLrel. 17, Created)
(TTEMBLrel. 17, Last sequence update)
(TTEMBLrel. 17, Last annotation update)
ryo cDNA, RIKEN full-length enriched lib
162L12, full insert sequence.
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                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                       Chordata;
Rodentia;
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20.7%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                           KNCHVLECIPGSI
                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          -GNLKMLRYLNLSGTGITVLPS
                                                                                                                                                          library
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kohdo S., Yamanaka I.
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kohdo S., Yamanaka I.
RA Kadota K., Watsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Watsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Cewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
Sato K., Wang K.H., Watzarelli J., Mombaerts P.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Haysshiraki Y.,
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                                                                              Q29433 PRELIMINARY;
Q29433;
Q1-NOV-1996 (TIEMBLITEL 01,
Q1-NOV-1996 (TIEMBLITEL 08,
Q1-NOV-1998 (TIEMBLITEL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
-I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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  Eukaryota;
                                                             Apolipoprotein B (Fragment)
                      scrofa
                                                                                                                                                                                                                                                                         273 IN 274
                                                                                                                                                                                                                                                                                                                 284 VD 285
                                                                                                                                                                                                                                                                                                                                                             219 RKLL---EGEESRISLPLPTFSSLNLRETNLESLPLVDTHSKRTL---LIKTVETRDGQV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VGAEAQEEFLRVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLS 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ----EGLESRFQSKSGYLRY-----SCESRIR----SYLREVSSYPST 177
                                                                                                                                                                                                                                                                                                                                                                                                    238 RHSINPYSNRESRI-----LFSTWNLDHI------IEKKRTIIPTLVEAIKEQDGRE 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QELQAQIQEQHVQIDVDVSKPDLTAALRDVRHEY-ESVAAKNLQEAEEWYKSKFADLSEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 QLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQV 97
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0038; filament; 1.
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(Pig).
Metazoa; Chordata; Craniata;
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20.2%; Pred. No. 0.27;
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                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                       PRT;
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                                                                                                                                                                       1540 AA
    Vertebrata;
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    Euteleostomi;
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RESULT 11
Q9U786
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MEDLINE-89108006; PubMed=2905687;
MEDLINE-891018006; PubMed=2905687;
Maeda N., Ebert D.L., Doers T.M., Newman M., Hasler-Rapacz J.,
Attie A.D., Rapacz J., Smithies O.;
"Molecular genetics of the apolipoprotein B gene in pigs in relation
"Molecular genetics of the apolipoprotein B gene in pigs in relation
to atherosclerosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
NCBI_TaxID-9823;
                                                                                                                                  REP3 OR DREP3 OR CG8364.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Trac

Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                    O9U786; PRELIMINARY; PRT; 266 AA.
O9U786;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to atherosclerosis.";
Gene 69:213-229(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maeda N., Ebert D.L., Doers T.M., Newman M., Hasler-Rapacz J., Attie A.D., Rapacz J., Smithles O.; Mattie A.D., Rapacz J., Smithles O.; Smithles O.; Bene in pigs in relation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 70:213-229(1988).
                                                                                                                                                                                                      DREP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                               Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                   MEDLINE-20085845;
                                                                   SEQUENCE FROM N.A.
 Inohara N., Nunez G.;
Genes with homology to DFF/CIDEs found
lell Death Differ. 6:823-824(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1166 RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKALK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ATDFASQLSSQVEQFVQE---DIQEYLSILADADGKGKEKIAELSSRAQEII-KSWAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAKGGSRLCTPEGWFSCQGPFDMDSCLS-----RHSINPYSNRESRILFSTWNLDH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSYLREVSSY------PSTVG-----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEELTRLKEKKLADFINDIQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEFIQNTLWEA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DEQAPORORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----
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1540 AA; 174656 MW; 1E67510A18582F0E CRC64;
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                                                 PubMed=10627165;
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19.5%;
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                                                                                                                                                    Tracheata; Hexapoda;
                                                                                                                                      Diptera;
                   'n
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                   Drosophila melanogaster.";
                                                                                                                                      Brachycera;
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Best Local
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EMBL; L11235; AAA74655.1; -.
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01-NOV-1996 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q29021
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InterPro; IPR003508; CAD.
Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
                                                                                                                                                                                                                       InterPro; IPR000510; Oxred_nitrognse1
Pfam; PF00148; oxidored_nitro; 1.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                            Q29021;
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                                                                                                                                                                         ry Match
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NON_TER
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Sturley S.L., Kodo
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 SQELQQLHQYIKALRKEYFDPSMVGWTVKYYELEEKVINLIKNLVDVLK--DFHSKYTVS
                  RSYLREVSSY------PSTVG----AEAQEEFLRVLGSMCQRLRSMQYNGSYFDR
                                      EEELTRLKEKKLADFINDIQQNINTTFNIYAPLGFRLLKENLDSPFGMLNEFIQNTLWEA
                                                       -DEQAPQRORLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGYLRYSCESRI---
                                                                            IKFTFDSVKYQLTDVVSEYGEQLKSLSQDVQKALSDLHSINITEILSELQIFLEGIFQEI
                                                                                                                RFQLPGRARNYTGDELCNMVMTEVGEVLSQIYSKIHSGLEILLSYFQDLMEKSKLNKARK
                                                                                                                                  REQLPER----GSRLC------LY---EDGTELTEDYFPSVPDNAEL----
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                                                                                              ------VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLC-----
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25.5%;
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nni V., Grunwald K., Nevin D.N., l
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Pred. No. 1
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Sus.
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RESULT 13
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Best Local S
Matches 89
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McClelland M., Sanderson K.E., Spieth J., Clifton S.W.
Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., N
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MEDLINE-21534948; PubMed-11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete genome sequence of Salmonella
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                                                                                                                                                                                 YLREVSSYPSTVGAEAQEEFL--RVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWF
                                                                                                                                                                                                                                                                                            SLLVLAGAGSGKTSVLVARAGWLLARGQADAGQILLLAFGRKAAEEM--DERIRERLHTE 268
                                                                                                                                                                                                                                                                                                                                                                                                        COEVLRKGCLRFQLPERGSRL---CLYEDG-TELTEDYFPSVPD---
EFQDISPQRAALLEALRKQNSQTTLFAVGDDWQAIY--RFSGAQLSLTTAFHQTFGEGEH
                                                                     ECRELFGKRIKLMAPLLKAWKSALKAENAVDFS--GLIHQAMVILEKGRFISPWKHILVD
                                                                                                        SCOGPFDMDSCLSRHSINPYSN---RESRILFSTWNLDH----IIEKKRTIIP-----
                                                                                                                                               WLEEEMQWVVPEGNFWDDETLQRRLAPRLDRWVSLMRMHG-----GAQAEMIAGAPE---
                                                                                                                                                                                                                    EITARTFHSLALYI-IQQGSKKAPVVSKLESDATARHQLFLRTWRQQCSEKKAQAKGWRQ 327
                                                                                                                                                                                                                                                         RLLADLLHNVSQNIAAETRAEDPPWFEGLES----RFQSKSGYLRYSCESR-----IRS
                                                                                                                                                                                                                                                                                                                                VLLTLGQAWQGYVSDI----RRFLSAFHEPQVGLI-----QAAQQLLCDEQAPQR---Q
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                                -TLVEAIKEODGREV-----DWEYFYGLLFTSENLKLVHIV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 98.5; DE Pred. No. 3.1; 52; Mismatches
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Mulvaney E.,
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RESULT 14
Q8Z7R7
ID 08Z7R
AC Q8Z7R
AC Q8Z7R
DT 01-MA
DT 01-MA
DT 01-JU
DE Helic
GN STY10
   RESULT 15
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Best Local S
Matches 89
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicase;
SEQUENCE
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Q8Z7R7;

01-MAR-2002 (TrEMBLrel. 20; Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Helicase IV (75 kDa helicase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              328 WLEEEMQWVVPEGNFWDDETLQRRLAPRLDRWVSLMRMHG-----GAQAEMIAGAPE--- 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496
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                                                                                      496 CHLDTTYREN---SRIGDIANREVQQNP 520
                                                                                                                                                 306 CHKKTTHKLNCDPSRIYKPQTRLKRKQP 333
                                                                                                                                                                                                         438 EFQDISPQRAALLEALRKQNSQTTLFAVGDDWQAIY--RFSGAQLSLTTAFHQTFGEGEH 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 YLREVSSYPSTVGAEAQEEFL--RVLGSMCQRLRSMQYNGSYFDRGAKGGSRLCTPEGWF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 EITARTFHSLALYI-IQQGSKKAPVVSKLESDATARHQLFLHTWRQQCSEKKAQAKGWRQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 RLLADLLHNVSQNIAAETRAEDPPWFEGLES----RFQSKSGYLRYSCESR-----IRS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 SLLVLAGAGSGKTSVLVARAGWLLARGQADAGQILLLAFGRKAAEEM--DERIRERLHTE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 CREIWRK-CLAWLQDSEGSROQHNQAYADAMLEAHADFFTQIESSPLNPSQARAVVNGES 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL627269; CAD08201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 VLLTLGQAWQGYVSDI----RRFLSAFHEPQVGLI-----QAAQQLLCDEQAPQR---Q 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 CQEVLRKGCLRFQLPERGSRL---CLYEDG-TELTEDYFPSVPD-----NAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                               ECRELFGKRIKLMAPLLKAWKSALKAENAVDFS--GLIHQAMVILEKGRFISPWKHILVD 437
                                                                                                                                                                                                                                                                                                                                                                                          SCQGPFDMDSCLSRHSINPYSN---RESRILFSTWNLDH----IIEKKRTIIP-----
                                                                                                                                                                                                                                                                    -----TLVEAIKEQDGREV-----DWEYFYGLLFTSENLKLVHIV-----
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22.9%; Pred. No. 3
7ative 52; Mismatche
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DRRRRRNOOCOONE E PACE
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AC O66

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Best Local S
Matches 58
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Q62238;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sex-limited protein Slp(w7) alpha-gamma chain (Fragment).
Mus musculus (Mouse).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  060819
                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 (Fragment).
CLCN6.
                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 20, Last annotation update)
DJ934G17.1.2 (Chloride chanel protein CLC-6B) (Isoform
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL021155; CAA15952.1; -.
                           Errington H. Submitted (1
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EMBL; X06454; CAA29760.1; -.
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MEDLINE-86176748; PubMed-3008092;
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                                                                                      SEQUENCE FROM N.A.
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InterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 G 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 -----ESRIRSYLREVSSYPSTYGAEAQEEFLRYLGSMCQRLRSMQYNGSYFDRGAK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 LATL---CSGDVCQCAQGKCPPLLRSLERRVEDKDGYRMRFACYYPRVEYGFTVKVLRED 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LADLLHNVSQNIAAETRAEDPPWFEGLESRFQSKSGY-LRYSC------ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 KLGLSGMAIADITLLSGFHALRGDLEKLTSLSDRYVSHFETDGPHVLL-YFDSVPTTREC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 KFGVAGRSCQEV-LRKG--CLRFQLPERGSRLCLY----EDGTELTEDYFPSVPDNAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 VLLTLGQAWQGYVSDIRRFLSAFHEPQVGLIQAAQQLLCD------EQAPQRQRL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.5%; Score 98; DB 11; Length 594; Similarity 24.1%; Pred. No. 2.8; Indels 69; Conservative 29; Mismatches 82; Indels
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594 P
66454 MW;
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POTENTIAL.
; 9465C569D9A37768 CRC64;
                                                                                                                                                                          Craniata; V
Catarrhini;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
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                                                                                                                                                                                                         Vertebrata; Euteleostomi;
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECUENCE F. MOOD G.E., Almeida N.F. Jr., WOO L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Palmleri A.,

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Fomero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

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Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

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Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

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Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P., Gordon

Kutyarin T., Levy R., Li M.-J., McClelland E., Famero P.
"Genome sequence of the plant pathogen Agrobacterium tumefaciens C58."; Science 294:2323-2328/2001
                                                                                                                       Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., M. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon-Kamm B., Liao L., Kim S., Hen Chumley F., Tingey S.V., Tomb J.-F., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetolactate synthase.
ATRC OR ATU5123 OR AGR_PAT_179
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Pfam; PF00654; voltage_CLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2317-2323(2001).
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01-NOV-1998
01-MAR-2002
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SEQUENCE
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088305;
                                                                                                                Pfam; PF00207; A2M; Pfam; PF01759; NTR;
                                                                                                                                                    Submitted (JUN-1998) to the EMBL/GGEMBL; AB015623; BAA31154.1; -.
InterPro: IPR001599; MacrogloblnA2
InterPro: IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                      STRAIN=F1 ANIMALS
Matsumoto K., Ikut
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EMBL; AE007884; AAK90497.1;
Plasmid; Complete proteome.
SEQUENCE 571 AA; 62030 M
                                                                                                                                                                                                                                  hydroxylase (Cyp21), and and complete sequences.";
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sex-limited
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                      Mus musculus 5' truncated
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Eutheria;
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  Conservative
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                                                                                                                                                                                                                                                                                          Ikuta
                                                                            AA;
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Rodentia;
                                                                            43649 MW;
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                5.3%;
27.6%;
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21;
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Last
Score 95; DB
Pred. No. 2.9;
21; Mismatches
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Sciurognathi; Muridae;
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                                                                            EE2AA97B15597047 CRC64;
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No. 3.
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2.9;
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62;
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48;
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OL-JUN-2002 (TrEMBLrel. 21, C1
Ol-JUN-2002 (TrEMBLrel. 21, L4
Ol-JUN-2002 (TrEMBLrel. 21, L4
      Q02689
Q02689;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
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EMBL; AB003040; BAB85589.1;
SEQUENCE 1572 AA; 178396
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21160571; PubMed-11260267;
Kohda T., Asai A., Kuroiwa Y., Kobayashi S., Aisaka K., Nagashima G.
Koshida M.C., Kondo Y., Kagiyama N., Kirino T., Kaneko-Ishino T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
63; Conserv
                                                                                                                                                                                                                                                                                                       ---RFPRPNDNWKDSSSSRRESVIQE-RGYEGS----AFRGGFRFNADLASRSRALERKR 268
                                                                                                                                                                                                                                                                                                                                        LESRFQSKSGYLRYSCESRIRSYLREVSSYPSTVGAEAQEEFLRVLGSMCQRLRSMQYNG 204
                                                                                                                                                                                                                                                                                                                                                                                                          PQVGL-----IQAAQQLLCDEQAPQ---RQRLLADLLHNVSQNIAAETRAEDPPWFEG 144
                                                                                                                                                              VCDECGRQFSVISEFVEHQ------IMHTRENLYEYGESFIHSV 363
                                                                                                                                                                                                                                 RYHFDSDERGSGHEHKSCVRKKPFECGA--EMRQAMSMGNLNSPSFSESQSI-DFWANPY 325
                                                                                                                                                                                                                                                                  SY-FD---RGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSINPYSNRESRILFSTWNLDH 260
      (TrEMBLrel. 01,
(TrEMBLrel. 01,
(TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178396 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%; Score 94; DB 11; Length 1572; 21.7%; Pred. No. 24; tive 47; Mismatches 118; Indels 6
Created)
Last sequence update)
Last annotation update)
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Search completed: May 26, Job time : 68 secs

2003, 15:22:58

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Best Local S
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SEQUENCE 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X55026; CAA38788.1; -.
InterPro; IPRO01982; Endonuc_LAG/HNH.
InterPro; Pf00961; LAGLIDADG_1; 2.
Hypothetical protein; Mitochondrion.
SEQUENCE 397 AA; 45576 MW; 6D736E89C2D15A7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
"The complete DNA sequence of the mitochondrial genome of Podospora
anserina.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90291512; PubMed-2357736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLETE MITOCHONDRIAL GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                          189 -----VLGSMCQRLRSMQYNG--SYFDRGAKGGSRLCTPEGWFSCQGPFDMDSCLSRHSI 241
                                                                                                                                                                                                                                                                                                                                                      163 DGDGCFQVSKKGYASLEIVTQLRDKRILYLIK-QKYGGAVKLHAGDNYLRYRLHHKAGLL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 17:375-402(1990).
x55026; CAA38788.1:-
275 --YLNEKSGQIFITAS-----QKNRFTLDALVELYGGTIYAMVKQD 313
                                                                                           242 NPYSNRESRILFSTWNLDHIIEKKRTIIPTLVE-----AIKEQD 280
                                                                                                                                                                             222 SLINGINGLIRNPIRILQLGKICNLYDIKLKDTQPLTYYNGWLS--GFFDTDGSI----
                                                                                                                                                                                                                                                                                                                                                                                                                                             151 -----SKSGYLRYSCESRIRS----YLREVSSYPSTVGAEAQEEFLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 FALLQYSIRLEKGYFLMKNLKYSTLASDYSENSLANTRNKNNSPFKEKEDRFNEWLAGII 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 QAAQQL----LCDEQAPQRQRLLADLLHNVSQNIAAETRAEDPPWFEGLESRFQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 KILVIMDNPQITKARSENYKPGITEFLGLCM-----WVGISEAIRLLPTSLSKKIKDLI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 RLCLYEDGTELT----EDYFPSVPDNAELVLLTLGQAWQGYVSDIRRFLSAFHEPQVGLI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2%; Score 93.5; DB 8; Length 397; 22.4%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 112; Indels
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SUMMARIES

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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -Q-Cgn2_1/USTO_9001/USO9748431/runat_21052003_153829_16273/app_query.fasta_1.519
-Qs-Cgn2_1/USTO_9001/USO9748431/runat_21052003_153829_16273/app_query.fasta_1.519
-DB-N_Geneseq_1011002 -QFMT=4stap -SUFFIX=rng -MINKATCH+0.1 -LOOPCI-0
-LOOPEXT=0 -UNITS-blts -STRAT=1 -END--1 -MATRIXX=blosum62 -TRRNS-human40.cdi
-LIST-45 -DCCALIGN-200 -TRR_SCORE-pct -TRR_MX-100 -TRR_MIN-0 -ALIGN-20
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MILEN=0 -MAXIEN=200000000
-USER-USO9748451_eCGN_1_1_263_erunat_21052003_153829_16273 -NCPU-6 -ICPU-3
-NO_MARP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBICKE-100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_INEGUT=30 -THREADS-1 -XGAPDP-10 -XGAPEXT-0.5 -FGAPOP-6
-DEV_TIMEOUT=120 -WARN_INEGUT=0.5 -DELOP-6 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ng table:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_101002:*

| N_GENESET_TYGGUTTA_yeneseq_/geneseqn-embl/NA1980.DAT:*
| N_GENESET_TYGGUTTA_yeneseq_/geneseqn-embl/NA1981.DAT:*
| N_GENESET_TYGGUTTA_yeneseq_/geneseqn-embl/NA1982.DAT:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May 26, 2003, 15:23:03; Search time 297 Seconds (without alignments)
2562.880 Million cell updates/sec
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1789
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AAS90919	AAS68767	AAA27121	AA542/32	MAS42/31	AAX91408	AAX91409	AAI59522	AAS98203	AAK51986	ABL29498	AAZ48766	AAK52970	ABL14003	AB000136	ABQ/3089	AAS84561	ABK52796	AAQ44511	AAQ51296	AAD26400	ABK44209	AAC64226	ABL14002	ABI99777	ABN51606	AAS948/3	AAA09307	AAA81540	AAA81490	AAF21607	ARKS4763	AAZ15100	ABL15179	AA189481	AAZ21180	AAZ21173	AAZ38992	AAX19907	AAD02498	AAH74642	Đ
encoding	coding	Human Adipose Spec	Keverse comprehence	Towns acms const		MGIS4 -	man polynucieo	DNA encoding plako	Human polynucleoti	Drosophila melanog	D. melanogaster DR	Human polynucleoti	Drosophila melanog	Himan Octooblact d	Himan nervous syst		Rabbit haem-regula	Haem-regulated euk	eIF-2 alpha kinase	5	cDNA #149 encoding	Human pollinosis-a	70	Mouse ischaemic co	20 6	Porcine acylglucos	Human vimentin cod	N. meningitidis pa	N. meningitidis B	Neisseria meningit	Human cDNA differe						Human DNA fragment	Caspase activated	₩.	Nucleotide sequenc	Description

RESULT 1
AAH74642
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XX AAH74642; Human; DNA fragmentation factor; DFF40; DFF45; apoptosis; DNase; molecular chaperone; cancer cell; ss. Nucleotide sequence of human DNA fragmentation factor 40 (DFF40). 15-OCT-2001 (first entry)

AAH74642 standard; cDNA; 2839 BP.

ALIGNMENTS

Homo sapiens. Location/Qualifiers 132..1148 /*tag= a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
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Human; DNA fragmentation factor; gene therapy; hyperproliferative psoriasis; angiogenesis; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying modulator of human DNA fragmentation factor 40, for treating cancer, involves contacting cell or cell-free composition comprising DFF40 with candidate substance and comparing apoptosis with
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06-JAN-1998;
22-AUG-1997;
22-AUG-1997;
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                                                                                                                                                                               New isolated caspase activated nuclease which can inhibit or activate apoptosis heart attack, stroke or tumours
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P-PSDB; AAY04123.
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The present sequence encodes a caspase activated nuclease (CPAN). Active CPAN proteins can be used for identifying compounds which inhibit apoptosis. Inhibitors of apoptosis can be used therapeutically, e.g. where cells are damaged and the apoptotic pathway is initiated such as by heart attack or stroke. The inactive CPAN proteins can be used for

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Alignment S Pred. No.:

Sequence 2839

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11 other;

Score:

Percent Similarity: Best Local Similarity:

9.26e-174 1763.00 98.82% 98.82%

Length:
Matches:
Conservative:
Mismatches:

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                        The present sequence encodes a human DNA fragmentation factor, designated DFF40. Also described are: (1) a method of inducing apoptosis in a cell comprising providing the cell with DFF40 which results in apoptosis; (2) a method for inhibiting the growth of a cancer cell comprising contacting a cancer cell with a DNA fragmentation factor designated DFF40 under conditions permitting the uptake of the DNA fragmentation factor by the cell where the presence of the DFF40 into the cell induces apoptosis; (3) a method for treating cancer comprising: (a) encoding a DFF40 DNA fragmentation factor, and (b) a promoter active in the tumour cell, where the promoter is operably linked to the region encoding the DNA fragmentation factor, under conditions permitting the uptake of the nucleic acid by the tumour cell; (4) a method of identifying a modulator of DFF40; and (5) a method of producing a functional DNA fragmentation factor. An expression construct encoding a DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. The expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor. An expression construct encoding a C DNA fragmentation factor.
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                                                                                                                                                                                                                                                                                                                                                                                               Page 125-127;
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                                      IleTyrLysProGlnThrArgLeuLysArgLysGlnProValArgLysArgGln 338
                                                                                           CTAGTGCACATTGTCTGCCATAAGAAAACCACCCACAAGCTCAACTGTGACCCGAGCAGA
                                                                                                                                                                 GGAAGAGAAGTGGACTGGGAGTATTTTTATGGCCTGCTTTTTACCTCAGAGAACCTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an inhibitor (ICAD) for caspase-activating DNase (CAD). Two ICAD's are specifically claimed: a long chain form (ICAD-L) and a shorth chain form (ICAD-S). ICAD and ICAD can be used in the prevention of cell death, and can be used as a research reagent for cell death. The present sequence encodes mouse CAD which is used in the exemplification of the present invention.
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P-PSDB; AAY29931.
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                     ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80
                                                                                                                                            GTGGCGGCCCGGAGCTGCCAGGAGCTGCCTAAGGGCTGCGTTCCCAGCTCCCG
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                              GluAlaGlnGluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMet
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            GCAGCTCAAGAAGAGTACCTGCGAGTCCTTGGCTCCATGTGCCAGAAGCTCAAATCGGTG
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO000010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                               07-SEP-2001.
                                                                        Claim 1; SEQ ID NO 9541; 1399pp + Sequence Listing; English.
                                                                                                                                     WPI; 2001-514838/56.
P-PSDB; AAO09550.
                                                                                                                                                                   Tang YT, Liu C, Drmanac RT
                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Venter JC,
                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
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11-JUL-2000; 2000US-0614150
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Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form specification, but was obtained in electronic i
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)B; ABB71076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                                                          GlnArg---GlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAla
                                                                                                                                                                                                                                                    CAATCGCCTTTGCTAAAGGTGGCT---GACATTTTCTACGATTTTATCGAACAGCATCCG
ACCCGCAATCCCTTGTACCGCCAAAATGCCAAGGCCCGACAAGTGATAAACTCTGTGCTG
                        LeuArg---
                                                                                                 GAGCGCTTCCACTCTAAGGAGGAAGCTATGGCCACACGTGCCCCAGACACGTGTGCGAGGC
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                                                                                                                                                                                                                                                                                                                                                         GACGATGAGTACTTAAAAAGCCTACCC-----
                                                                                                                                                                                                                                                                                                                                                                                GluAsp----TyrPheProSerValProAspAsnAlaGluLeuValLeuThrLeuGly
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                                                                        TyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPhe
                                                                                                                          SerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSer
                                                                                                                                                   AACAGCAAGACCCACCTCAGCTTAAAGGCCGAGCACGTGGAGTGGTTCACGGGCGGCGAG
                                                                                                                                                                             GluThr-
                                                                                                                                                                                                                                                                            GlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAsp-----GluGlnAlaPro 113
                                                                                                                                                                                                                                                                                                      CCG-----GATGCAGTCATTACAACAGATGCCGATTTTGAGTTTGAGAAGATGCGACAA
                                                                                                                                                                                                                                                                                                                              GlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAlaPheHisGluPro
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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(HYSE-)
                                                                                                                                                                                                                                      genetic analysis; c
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detection; m
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                     CHIRON
HYSEQ 1
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apping; tissue typing; pro
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                                                         98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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Crkvenjakov R, Dickson
Escobedo J, Garcia PD,
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M, Drmanac
Garcia V,
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CC comprising the sequences given in ARXI2532 to ARXI779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, and CC mapping, tissue typing or profiling, forensics, genetic analysis and CC can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct CC arrays for diagnostics (which may be used to determine function of an CC two cells (e.g. to identify abnormal or diseased tissue in a human, to CC cancer). The polynucleotides of the susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC cancer). The polynucleotides of the invention are especially used in the CC cancer). The polynucleotides of the invention are especially used in the CC cancer). The polynucleotides can also be used to screen for CC peptide analogues and annagement of colorectal cancer, breast cancer, CC and lung cancer. The polynucleotides can also be used to screen for
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ABL15178/c
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Lamson G, Leshk
Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 735 BP; 141 A; 189 C;
                          ABL15178 standard; cDNA; 3758 BP
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                                                                                                                                                                                                           574 AGCCGGATCCCGAGTTACCTGAGGGANGTGAGCTCCTA-CCNTCCACGGTGGGTGCGGAG
                                                                                                                                                                                                                                                                                                     515 NTTGAAGC-TTGGAGTTNCGATTTCANAGCANGTNTGGCTATCTGANATACANCTGTNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 ValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGln 101
                                                                                                                                                                                                                                SerargIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGlu
                                                                                                                                                             AlaGlnGluGluPhe------LeuArgValLeuGlySerMetCys 194
                                                                                                                  NCTAA-GAGGAATTCTGCGGTCTTGCTCATTGCAGAGCTCCGTCATCATCATGC 685
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Leshkowitz D, Pot D, Randazzo F, Re
in B, Sudduth-Klinger J, Williams LT;
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16.96%
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                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling (cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABJ16176-ABJ30511), expressed DNA sequences (ABJ16180-ABJ16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; deve
pharmaceutical;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 40016.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3758
                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 40016; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                2230 CCTCGTTATAATTCGGCCATGTCAAGGGCATTACAA-----TTAAATCGTTTTTTTTT 217:
                                                                                                                      2176 ACCTTTTAGCTTCTCGAG-----CCACATTTGTATTTGGCTTCTGATGGCTTCGAGGTG 2123
2122 TCCGACGATGAGTACTTAAAAAGCCTACCCGCCCAGACGCTGTTCATAGTGTCTGGCCCG 206:
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                              71 -----LeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer------AspIle
                                                                                      56 ThrGluAsp---TyrPheProSerValProAspAsnAlaGluLeuVal----
                                                                                                                                                                                                            16 ProArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeu 35
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2000US-0614150
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                                                                                                                                                                         LysLeuAsnCysAspProSerArgIleTyrLys 323
                                                                                                                                                                                                                                               LeuLysLeuValHisIleValCysHisLysLys------
                                                                                                                                                                                                                                                                                                                                         ArgGluValAsp-----TrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsn 298
                                                                                                                                                                                                                                                                                                                                                                                                   GTTGCAAATGTGGAAGAACTTGTGAGTCATCCGCAGACCAAGTGTTCAATTCATAAGAAG 1199
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                                         CDNA;
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14-AUG-2002 (first entry)

differentially expressed in granulocytic cells #1334.

adult respiratory distress syndrome; inflammatory bowel d Crohn's disease; ulcerative colitis; periodontal disease; rheumatoid arthritis; glomerulonephritis; asthma; thro cardiac reperfusion injury; renal reperfusion injury; viral infection; parasitic infection; |
fungal infection; sterile inflammatory ; ss; granulocytic cell; DNA chip; bacterial infection; infection; parasitic infection; protozoal infection: disease; psoriasis; thrombosis; bowel disease;

Homo sapiens.

WO200228999-A2

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11-APR-2002

03-OCT-2001; 2001WO-US30821

03-OCT-2000; 2000US-237189P

(GENE-) GENE LOGIC INC

Beazer-Barclay Y, Weissman XX, Yamaga ß Vockley

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and

Claim 1; SEQ ID No 1334; 114pp; English

GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation; especially chronic) or in a tissue, or sterile inflammatory disease, by contacting a tissue having reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, alcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and Missequence represents a gene differentially expressed in granulocyt Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. Mi is useful for detecting GCA, M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, rena. (GCA), by detecting the level of expression of gene(s) DNA chip analysis as given in the specification, and counter expression level to an expression level in an unac-The invention relates to detecting (M1) granulocyte n, and comparing an unactivated (GC) in granulocytes part (GS) identified Ж5 (M3) уd

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Db Qy	Ov Db	Qy	Db Qy	Db 49) D	V	₽ 4g	Db Qy	Qy Db.	ОУ	Qу	Qу	Db		-2	Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local S Query Match:	xx SQ Sequ
CTCAATGTTAAGATGCCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTG TyrSerAsnArgGluSerArgIleLeu	1275GACCTG	4 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp	184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn ::: ::: :::	1164 GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGCCGCCTGCAG	4 TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG	CCTCACC	139 FIGHTOITEPINE	LeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAsp 	GlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeu	84 ASPILeArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla :::	64 ProAspAsnalaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer	44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal	24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly :: :: 682 AGAAATTGCAGG	4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly	Gaps:	Scores: 0.00755 124.50 milarity: 34.70% Similarity: 21.59% h: 6.96%	equence 1851 BP; 489 A; 525 C; 472 G; 365 T; 0 other;
1334 255 1391	1280	223	203 1274	1220	1163	158 , 1103	1043	138 983	118 · · · · · · · · · · · · · · · · · ·	103	83 809	63 . 749	43 693	23 681			
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The present invention describes the full length genome of Neisseria meningitidis B (NNB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NNB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (1.e. the last 49980 bp of AAF21547 are repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins given in AAS58550 to AAS58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NNB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the
                                                                                                                                                                                                                                                                                                                                                                                    Pizza M, Hickey E, I
Galeotti C, Mora M,
Frazer CM, Grandi G;
                                                                                                                                                                                                                                                         Claim 7; Appendix A; 692pp; English.
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08-OCT-1999;
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99WO-US23573.
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Ratti G, Scarselli M,
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Scarlato V,
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Rappuoli R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins can be used in compositions for treating or preventing infect due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computationabases can be used in a search to identify open reading frames (ORF or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which
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                             leAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisI 261
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TGAATCCTTATCGAAACCGAACAGGGTTTTGGCAGAĈAGGGAAATGGTTTCATCAACATA

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AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA81490
                                                                                                                                                       Neisseria DNA sequences and their corresponding proteins; AAA81254
AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                   The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
                                                                                                                                                                                                                                                                                  Claim 7; Page 866-1272; 1760pp;
                                                                                                                                                                                                                                                                                                               other Neisserial infections, for example,
                                                                                                                                                                                                                                                                                                                              Isolated nucleotide sequences of Neisseria used in the diagnosis and treatment of N.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-318079/27.
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30-APR-1999;
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C, Mora
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Scarselli
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                                                                                                      385893 ------GCGCCAATA---CTTTCAGGTTGTCTTGAGCTTCGGCGCGCAA 385854
                                                                                                                                                                                                      385919 TT---GGACATTGGTTCGACTCAGGCGTT------
385853 TGAATCCTTATCGAAACCGAACAGGGTTTTGGCAGACAGGGAAATGGTTTCATCAACATA 385794
                                                                                                                                                                                                                                                                                                                                                      188 rgValLeuGlySerMetCysGlnArg-------------------LeuArgSerMetGlnT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 euArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGlnGluGluPheLeuA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 lnAsnIleAlaAlaGluThrArgAlaGluAspProProTrpPheGluGlyLeuGluSerA 148
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                                             241 leAsnProTyrSerAsnArgCluSerArgIleLeuPheSerThrTrpAsnLeuAspHisI 261
                                                                                                                                                                                                                                                   202 yrAsnGlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluG 222
                                                                                                                                          222 lyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSer---ArgHisSerI 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 GlyCys-----LeuArgPheGlnLeuProGluArgGlySerArgLeuCysLeu 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrL 168
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##888888888888888888888888888888888888	PI DR XX PFI PFI PFI PFI PFI PFI PFI PFI PFI PFI	PR XXX	XXX XXX XXX XXX XXX XXX XXX XXX XXX XX		Qy Db	P 04	Qy Qy	Ор
ent invention describes n from Neisseria genomic s; AAA81301 claimed Ne; AAA81303 and their specifically claimed Ne; AAA81304 to AAA81303 and AAS61304 to AAA81301 n of Neisseria meningitic represent Neisseria meningitic represent Neisseria meningitic represent Neisseria meningitic represent Neisseria meningi which are all used in the them, can be used in the them, can be used as a medint) for treating, prevential bacteria. For example, nents of vaccines against all pathogenic Neisbacterium will also faccines garry organism-specific pu	y, Galeotti C, Mora M, Ratti G, , Pizza M; 318079/27.	99WO-US23573. 98US-0103794. 99US-0132068. ON CORP.	dis partial D mingitidis; N ccine; diagnos cs B; MenB; ds nningitidis. A2.	14 40/c 40/c AA81540 standard; DNA; 782 BP. AA81540; A-DEC-2000 (first entry)	313 ysLeuAsnCysAspProSerArgIleTyrLysProGlnThrArgLeuLysArgLys 331	295 hrSerGluasnLeuLysLeuValHisIleValCysHisLysLysThrThrHisI 313	275 laileLysGluGlnAspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheT 295 ::: ::: ::: 1	261 leIleGluLysLysArgThrIleIleProThrLeuValGluA 275 ::: ::: ::: 385793 TTOCGGAGCCTGCTCCACAACGACGACACAGCGGGTGCGGGTTCGGGTTCTGGCTCGGG 385734

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          N1K1 Interacting Protein; vimentin; protein complex; antiviral; neuroprotective; cardiant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meningococcus B vaccines have failed mainly due to antigen tolerance multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system & which are not antigenically variable or at least more conserved than
                                                                            10-AUG-2000
                                                                                                        AAA09307
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                                                                                                                                                                                                                                                                                        CGGGGGCAGCAACCGCATCGCCGCATTCTACGCGAC----CTTGGCTTGCTTTATCAA
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                                                                                                                                                                                                                                                                                                        IleGlu-----
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                                                                                                                                                                                  TTACGGTGTAACCCTGAACGGACGCCTCGCCCGCAACAGCAGTGCCGGAAGCGA
                                                                                                                                                                                                                                      -GGACATTGGTTCGACTCAGGCGTT---------
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                                                                           (first entry)
                                                  coding sequence
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23.23%
5.87%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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671

GTTGACAATGCGTCTCTGGCACGTCTTGAACCCTTGAACGCAAAGTGGAATCTTTGCAAGAA 730

ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83

64

615

44

SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63

AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT

670

614

603

AGAAATTGCAGG

24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43

AAGCCCGCGTCG----AGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGG 601

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                           US-09-748-451-2 (1-338) x AAA09307
                                                      Query Match:
DB:
                                                                                  Best
                                                                                                                                                                    Percent Similarity:
                                                                                                                                       Alignment Scores:
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                                                                                  Local Similarity:
                                                                                                                                                                                                                            14-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2, IP-3, IP-4, or IP-5. NIK1 (also referred to as Nek2) is a human homologue of the Aspergillus nidulans mitotic regulator, NIMA kinase. NIK1 is a serine/threonine-specific kinase and is thought to play a k role in cell-cycle events leading to the onset of mitosis. The complexes, their derivatives and NIK1 or NIK1-IP protein and DNA sequences, etc. are useful for treating or preventing a disease or disorder involving aberrant levels of the complex or protein. Such
                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating cancer, neurodegenerative disorder, metabolic disorders
                                                                                                                                                                                                      disorders include cancer, hyperproliferative dineurodegenerative disorders, cardiomyopathies,
                                                                                                                                                                                                                                                                                                                                                         NLK1 protein and a NLK1 protein-interacting protein, where the
                                                                                                                                                                                                                                                                                                                                                                                                   AAA09303-09 were isolated in a modified yeast two hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 142-145; 172pp;
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                                                                                                                                                                 Sequence 1766 BP; 479 A;
                                                                                                                                                                                              metabolic
                                                                                                                                                                                                                                                                                                                                                                                      N1K1 protein
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                                                                                                                          No.:
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                                                                                                                                                                                                                                                                                                                               interacting protein is chosen from TrkA, protein phosphatase lalpha,
l4-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2,
                                                                                                                                                                                                                                                                                                                                                                         interacting proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex of a NLK1 protein and a NLK1 protein-interacting protein, ful for treating cancer, hyperproliferative disorder, rodegenerative disorder, cardiomyopathies, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-303742/26
DB; AAY92335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23
                                                                                                                                                                                              disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 7
                                                                                                                                                                                                                                                                                                                                                                     as "bait". These are known sequences which proteins. The invention concerns purified or
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                           (1-1766)
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                                                                                                                                                                 449 G;
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                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                           AAS94873 standard; DNA; 1939 BP.
                         cardiovascular disorder; coronary artery disease;
                                               Human; foam cell differentiation; atherosclerosis; cerebral stroke;
                                                                                               Human DNA sequence #128 expressed during foam cell differentiation.
                                                                                                                                              14-FEB-2002
                                                                                                                                                                                                                                                                                                                                       1484 GAATAAAAAAGAAATCCATATCTTA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1085 GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGC----CGCCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1142 GATGAGATTCAGAATATGAAGGAAGAATGGCTCGTCACCTTCGTGAATACCAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 1424 CATCACGATGACCTTGAATAAAATTGCACACTCAGTGCAGCAATATATTACCAGCAA 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1202 CTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCCACCTACAGGAAGCTGCTG----- 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           848 CTGCGTGACGTACGTCAGCAATAT---GAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCA 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 -----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               965 GCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACC 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr------ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 GAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGAC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ProProTrpPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 LeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAsp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          788 ATTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCC 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       731 GAGATT --- GCCTTTTTGAAGAAACTCCACGAAGAGGAAATCCAGGAGCTGCAGGCTCAG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243
                                                                                                                                                                                                                                                                                                                                                                                    297 uAsnLeuLysLeuValHisIleVal 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGAAACTAATCTGGATTCACTCCCTCTGGTTGATACCCACTCAAAAAGGACACTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TrpAsnLeuAspHisIle------IleGluLysLysArgThrIleIle 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrSerAsnArgGluSerArgIleLeu------PheSerThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GAAGGCGAGGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTCCTCCCTGAACCTG 1312
                                                                                                                                              (first entry)
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                            gene therapy; ds
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides are useful as a high the diagnosis of disorders associated with foam cell development such as atheroscierosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotide sequences can also be used useful in gene therapy. Assign the invention which are differentially expressent the human polynucleotide sequences of the invention which are differentially expressed.
                                                                                                                                                                                                                                                                                                                                                           Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                                                                                                                        Claim 1; Page 184-185; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010925/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shiffman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000US-195106P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Sequence 1939 BP; 514 A; 551 C; 490 G; 383 T; 1 other;
                                     expressed during foam cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somogyi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawn R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mikita
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Pred. No.: 1.61 Length: 1939

Pred. No.: 102.50 Matches: 77

Percent Similarity: 34.42% Conservative: 50

Best Local Similarity: 20.87% Mismatches: 128

Query Match: 5.73% Indels: 15

DB: 24 Gaps: 16

US-09-748-451-2 (1-338) x AAS94873 (1-1939)

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949	. 104	. 892	84	. 832	64	776	44	764	24	707	4
949 ATTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCC 1008	GlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeu 118	<u>AGAAACTCCACGAAGAAGGAAATCCAGGAG</u>	AspīleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla 103	8	64 ProAspAsnAlaGluLeuValLeuTeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83	776AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 831	SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63	764 AGAAATTGCAGG 775	24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43	:grcgaggtggagcgcgacaacctggccgaggacatcatgcgcct	LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23
.008	.18	148	.03	191	ଘ	131	نت	75	ω	63	ω _,

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Porcine; acylgiucos
N-acetylneuraminic
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122
AATO4122 standard; DNA;
                                                                                                                                                                                     Porcine acylglucosamine-2-epimerase DNA
                                                                                                                                                                                                                   09-MAY-1996 (first entry)
                 WO9526399-A1
                                                                                                              scrofa.
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1303 GATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
                                                                                                                                        acylglucosamine-2-epimerase;
neuraminic acid; renin-bindin
                                                                                                                                                                                                                                                                                                                                              GAATAAAAAAGAAATCCATATCTTA 1669
                                                                                                                                                                                                                                                                                                                                                                                                            CATCACGATGACCTTGAATAAAATTGCACACACTCAGTGCAGCAATATATTACCAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp------
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                                               D)
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                                                                                                                                      renin-binding; enzymatic
                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerGl 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SerCysGluSerArgIleArg------
                                                                                                                                                                                                                                                                                                                                                                             305
                                                                                                                                                        N-acetylmannosamine;
                                                                                                                                        production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -Glu 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT04122 encodes AAR79928 porcine acylglucosamine-2-epimerase with renin-binding activity. A2P can be used for the enzymatic prodn. of N-acetylmannosamine and N-acetylneuraminic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant acyl:glucosamine-2-epimerase with renin-binding - useful in enzymic production of N-acetyl:mannosamine and N-acetyl:neuraminic acid
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25-MAR-1994;
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DB; AAR79928.
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                                                                                                                                                       CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGAGGCACGGTACCAGAGCGAAGCG--
                                                                                                                                                                                  rArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGl 154
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                                                                                                                                                                                                                                                                                                                                                             CAAGTACGTCTGGCTGCAGGGGAGGCAGGTGTGGATG----TACTGTCGCCTGTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pages 55-56; 74pp; Japanese
-PheLeuArgValLeu-GlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlyS
                           GCTGGGCCGGCCCCAGCTCCCCGGGGCCGTGGCCTCGGAGTCCATGGCAGTGCCCATGAT
                                                                                                                      YTYrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer--
                                                                                                                                                                                                                                                                                                          -----LeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLe 123
                                                                                                                                                                                                                                                                                                                                           CAAGCTTGAGCGCTTCCACCGCCCTGAG-----CTTCTGGATGCGGCTAAAGCAGGGGG
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94JP-0056271
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                                                          -TyrProSerThrValGlyAlaGluAlaGlnGluGlu---
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           messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting RNAs from a plological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minitarins in the detect transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minitarins or the corresponding transcriptome.
                                                                                                                                                                                                         The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub\mbox{-})transcriptome, where the
                                                                                                                                                                                                                                                                                                   New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoshan A,
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02-MAY-2001;
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splice variant;
                                                                                                                                                                                                                                                                Example 1; SEQ ID 24354; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN INC
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2001US-287724P
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t; transcriptome; oligonucleotide library; ss.
transcripts of a sub-transcriptome under a
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                   Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular
                                                   Claim 2; Page 2174-2177; 2690pp; English.
                                                                                                                                                                        WPI; 2002-034733/04.
P-PSDB; ABB57310.
                                                                                                                                                                                                                       Ishikawa K, Asai S,
                                                                                                                                                                                                                                                                                                                             18-MAY-2001; 2001WO-JP04192.
                                                                                                                                                                                                                                                                                                                                                              22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ischaemic condition related cDNA sequence SEQ ID NO:866
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                                                                                                                                                                                                                                                           (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                             18-MAY-2000; 2000JP-0145977.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2174
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                                                                 PheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrpPheSerCys
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                                                                                                                               LeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyr 206
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                                                                                             The invention relates to an isolated nucleic acid detection reagent
                                                                                                                    Claim 1; SEQ
                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                     P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
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                                                                                                                  21pp +
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for elucidating cell signalling
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

is

The sequence data specification, but sequences (ABL0184) (ABB57737-ABB72072)

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                                                    219 ThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArg 238
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297 2197	279 2254	259 2295	239 2316
297 GluAsnLeuLysLeuValHisIleValCysHisLysLysThrThr 311 ::: :: ::: 2197 AGCAACACGGCACCATCGAGGTGGTGCAGTGCGACAATCAAAACACG 2150	279 GlnAspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSer 296 ::: :::	259 AspHisIleIleGluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGlu 278	239 HisserIleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeu 258 ::: ::: 2316 TGAAAGCTGGTGCCATTTTCT

Search completed: May 26, 2003, 16:31:19 Job time : 729 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-x1h
-O-/cgn2_1/USPTO_spool_US09748451/runat_21052003_153830_16303/app_query.fasta_1.519
-DB-Issued_Patents_NA -OPMT-fastap -SUFFIX-rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATKIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MO-0 -ALIGN-20
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-NOSER-US09748451_@CGN1_1_40_@runat_21052003_153830_16303 -NOPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/ina/5A_COMB.seq; *
/cgn2_6/ptodata/1/ina/5A_COMB.seq; *
/cgn2_6/ptodata/1/ina/6A_COMB.seq; *
/cgn2_6/ptodata/1/ina/6B_COMB.seq; *
/cgn2_6/ptodata/1/ina/backfiles1.seq; *
/cgn2_6/ptodata/1/ina/backfiles1.seq; *
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US-09-061-702-1
US-08-53-703A-5
US-08-53-703A-9
US-09-006-021-9
US-09-006-021-9
US-07-938-782A-1
PCT-US-08-630-524-1
PCT-US-08-630-524-1
US-08-630-524-1
US-09-069-023-21
US-09-065-1938-8
US-09-061-702-3
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1645.345 Million cell updates/sec
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Sequence 5,
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US-08-659-251-14 US-09-256-490-14 PCT-US96-11445-14 US-08-659-251-1 US-08-659-250-1	US-08-533-306A-5 US-08-742-92A-5 US-09-103-840A-2 US-09-103-840A-1 US-08-873-093-2 US-09-206-646-2	1056-1056-1056-1056-1056-1056-1056-1056-	3-1 069-023- 794-158- 794-158- 794-342- 069-023- 069-023- 069-023- 0707-7934- 707-7934- 707-7934-
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ALIGNMENTS

RESULT 1 US-09-061-702-1

sequence 1, Application US/09061702
Patent No. 6165737

INFORMATION:

APPLICANT: Wand, Xiaodong
APPLICANT: Liu, Xuesong
ITITLE OF INVENTION: APOPTOSIS
IUTHER OF INVENTION: APOPTOSIS
IUTHER OF INVENTION: APOPTOSIS
IUTHER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHOLD, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SOFTWARE: PATENTION: WOMBER: US/9/061,702
APPLICATION NUMBER: US/9/061,702
FILING DATE: Concurrently Herewith
CLASSIFICATION:
NAME: MCM1111an, Nabeela R.
REGISTRATION NUMBER: US/9/061
REGISTRATION NUMBER: US/9/06
TELEPHONE: (512)418-3000
TELEPHONE: (512)418-3000
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TELEPHONE: GST2)418-3000

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DB:
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Best Local Similarity:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                              GlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLys
                               IleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSer 240
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                                                                           ATCAACCCCTACAGTAACAGGGAGGAGCAGGATCCTCTTCAGCACCTGGAACCTGGATCAC
                                                                                                                     GAAGGCTGGTTCTCCTGCCAGGGTCCCTTTGACATGGACAGCTGCTTATCAAGACACTCC
                                                                                                                                                                                                                                                                                               TGGTTTGAAGGCTTGGAGTCCCGATTTCAGAGCAAGTCTGGCTATCTGAGATACAGCTGT
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-553-703A-5
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US-08-553-703A-5
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                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Ver
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Altman, Daniel E REGISTRATION NUMBER: 34,115 REFERENCE/DOCKET NUMBER: TELECOMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADUNESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA
                                                                                                                                                                                                                                                                           LENGTH: 1209 base pai
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                    LeuValHisIleValCysHisLysLysThrThrHisLysLeuAsnCysAspProSerArg
                        sLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerValProAspAsnAl
                                                                                                                                                                                                                                                                 TYPE:
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27.24%
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Matches:
Conservative:
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Indels:
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RESULT 3
US-08-553-703A-9
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                                                                                                                                                                                                                    APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                           ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
     COMPUTER: IBM Compatible
                                                                                                     COUNTRY:
                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 CTCCGGATGGGACGCTGATCAC 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 GCTGCTGTGCCTGGTGGAGCAGCTCGGGGAGGAGGAGGAGGAGCTGGCAGGCCGCTACGC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 -PheLeuArgValLeu-GlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlyS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 GCTGGGCCGGGCCCCAGCTCCCCGGGGCCGTGGCCTCGGAGTCCATGGCAGTGCCCATGAT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 -----TyrProSerThrValGlyAlaGluAlaGlnGluGlu------ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 -----GTGGACATGATGGATCAGATCGTGCACTGGGTGCGAGAGGACCCCTCTGG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 rArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGl 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 -SerThrTrpAsnLeuAspHis 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    669 GGCTGTGCTGGAGAATGTGTCGGAAGATGGCGAGGAACTTTCTGGCTGCCTGGGGAGACA 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 GCAGCTGGGGCACTGGTGCGCTCGGAGGATCC---TGCAGCACGTCCAGAGGGATGGACA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 erTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThr-ProGluGlyTrpPhe 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 yTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGAGGCACGGTACCAGAGCGAAGCG-- 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 CGAATTTTTGCTGCGCCATGCCCGAGTGGCACCTCCTGAAAAGAAGTGTGCCTTTGTGCT 323
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Best Local Similarity:
Query Match:
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US-08-553-703A-9
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SOFTWARE: FASTSEO VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,703A
FILING DATE: 30-NOV-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1209 base pairs
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NAME/KEY: Coding Sequence
LOCATION: 1..1206
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
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REGISTRATION NUMBER: 34,115
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                                                                                 154 yTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer-- 173
174 -----TyrProSerThrValGlyAlaGluAlaGlnGluGlu-----
                                                 442 ------GTGGACATGATGGATCAGATCGTGCACTGGGTGCGAGAGGACCCCTCTGG 491
                                                                                                                                                 384 CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGAGGCACGGTACCAGAGCGAAGCG-- 441
                                                                                                                                                                                                134 rArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGl 154
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                                                                                                                                                                                                                                                                                                                                                  264 CGAATTTTTGCTGCGCCATGCCCGAGTGGCACCTCCTGAAAAAGAAGTGTGCCTTTGTGCT
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-006-021-5
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                        TOPOLOGY: 1:
MOLECULE TYPE:
-09-006-021-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         APPLICATION NUMBER: 08/5
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                            STRANDEDNESS:
                                                                                                                                                                                  NAME: Altman, Daniel E REGISTRATION NUMBER: 34,115
                                                                                                                                     TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                    LENGTH:
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RESULT 5
US-09-006-021-9
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           Application US/09006021
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Percent Similarity:
Best Local Similarity:
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                                   -SerThrTrpAsnLeuAspHis 260
CTCCGGATGGGACGCTGATCAC
                                                                                  GAGCGGTGACGCCAAACTTCGAGCCCACGTCATCGACACGTTCCTGCTACTGCCTTTCCG
                                                                                                                                                                           CCAG----AACCCAGGCCACGCGCTGGAAGCTGGCTGGTTCCTGCTCCGCCACAGCAGCCG
                                                                                                                                                                                                                        sSerIleAsnPro--
                                                                                                                                                                                                                                                                    GGCTGTGCTGGAGAATGTCGGAAGATGGCGAGGAACTTTCTGGCTGCCTGGGGAGACA
                                                                                                                                                                                                                                                                                                               SerCysGlnGlyPro-Phe-----
                                                                                                                                                                                                                                                                                                                                                           GCAGCTGGGGCACTGGTGCGCTCGGAGGATCC---TGCAGCACGTCCAGAGGGATGGACA
                                                                                                                                                                                                                                                                                                                                                                                     erTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThr-ProGluGlyTrpPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGCTGTGCCTGGAGCAGCAGCTCGGGGAGGAGGACGAGGAGGAGCTGGCAGGCCGCTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGGCCATGAACGAGCTGTGGAGGGTGACGGCGGGGGGCACGGTACCAGAGCGAAGCG--
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                -----AspMetAspSerCysLeuSerArgHi
                                                                                                                              ---GluSerArgIleLeuPhe-----
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
GENERAL I
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SEQUENCE CHARACTERISTICS:
LENGTH: 1209 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/553,703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/5:
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 714-760-0404
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TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
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APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence
LOCATION: 1...1206
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                         210 CAAGCTTGAGCGCTTCCACCGCCCTGAG-----CTTCTGGATGCGGCTAAAGCAGGGGG 263
                                                                                                              156 CAAGTACGTCTGGCTGCAGGGGAGGCAGGTGTGGATG-----TACTGTCGCCTGTACCG 209
                                                                                                                                                                                                   123 CCTGGGCCGCGACGGG------
                                                                 87 gPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGln---- 105
                                                                                                                                                   67 aGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgAr 87
                                                                                                                                                                                                                                      47 sLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerValProAspAsnAl 67
                                                                                                                                                                                                                                                                                   63 CGTGATGGCTTTCTGGCTGGAGCACTCCCACGATCGGGAGCACGGGGGCTTCTTCACGTG 122
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Matches:
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US-07-938-782A-J
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,782A
FILING DATE: 31-AUG-1992
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Pabst, Patree L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07938782A Patent No. 5525513
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: London, Irving M.
TITLE OF INVENTION: DNA Encoding the Heme-Regulated
TITLE OF INVENTION: Eurkaryotic Initiation Factor 2 alpha kinase
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 rArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGl 154
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                                                                                                                                                                                                                                                          Georgia
Y: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PheLeuArgValLeu-GlySerMetCysGlnArgLeuArgSerMetGlnTyrAsnGlyS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGGGCCGGCCCCAGCTCCCCGGGGCCGTGGCCTCGGAGTCCATGGCAGTGCCCATGAT 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Jane J.
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                   Alignment Scores: Pred. No.:
US-09-748-451-2 (1-338) x US-07-938-782A-1 (1-2729)
                                                                                                                                                                                              US-07-938-782A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:

NAME/KEY: m1sc_featu
LCCATION: 543..560
OTHER INFORMATION: 0
OTHER INFORMATION: a
OTHER INFORMATION: u
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1009:.1031
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of a human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 448..468
OTHER INFORMATION: /not OTHER INFORMATION: ampl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI OTHER INFORMATION: mRNA in Human erythroid cells, using as the OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
OTHER INFORMATION: to 2149."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                            PAGES: 7729-7733
DATE: September-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 229..249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                               : London, Irring M.
Cloning of the cDNA of the heme-
regulated eukaryotic initiation factor
zalpha (eIF-Zalpha)kinase of rabbit reticulocytes:
Homology to yeast GCN2 protein kinase and human
double-stranded-RNA-dependent
: proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                     Chen, Jane J.
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543..560
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                                                          0.247
96.00
35.43%
20.53%
5.37%
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amplification of human HRI cDNA sequence
using the rabbit HRI cDNA sequence."
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                                     Conservative: Mismatches: Indels: Gaps:
                                                                                                                  Matches:
                                                                                                                                 Length:
                                     2729
62
45
121
74
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4 Lysprotysservaltysteakrglateakrglateakrglaphodlys
4 LysProlysSerVallysLeukrgSerProkygLysPheGlyvallalel 1427 AMGCCTMGAAATATTETTCTTCATGGTCCTGATCACAAGTGAAAATAGGAGACTTTGGT 24 ATGCCTAGAAATATTETTCTTCATGGTCCTGATCACAAGTGAAATAGGAGACTTTGGT 24 ATGCCTAGAAATATTETTCTTCATGGTCCTGATCACAAGTGAAATAGGAGACTTTGGT 24 ATGCCTAGAAATATTTTTCTTCATGGTCCTGATCACAAGTGAAAATAGGAGACTTTGGT 24 ATGCCTAGAAATATTTTTCTCAGAAAGAATGGAGACCAGCAGCAAGAAAAGGAGGAGAAA 31 LeuProGlukrgGlySerTxgLeu

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938
EILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: PABST, PATTER 1, 284
REGISTRATION NUMBER: WIIO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEPHONE: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2729 base pairs
TYPE: NUCLEY CALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/630,524
FILING DATE: 10-APR-1996
                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 543..560
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: using the rabbit HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PEATURE:
NAME/KEY: misc_feature
LOCATION: 448..468
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PEATURE:
NAME_KEY: misc_feature
LOCATION: 1009.1031
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of a human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 229:.249
OTHER INFORMATION: /note OTHER INFORMATION: using
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ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 113. 2149
OTHER INFORMATION: /note= "Expression of HRI
OTHER INFORMATION: mRNA in Human erythroid cells, using as the
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
OTHER INFORMATION: to 2149."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit
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amplification of human HRI cDNA sequence
using the rabbit HRI cDNA sequence."
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Best Local Similarity:
Query Match:
DB:
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TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: September-1991
                                                                                                                                                                                                                                                                                1979 GAGCTCCCTGCCTAGCCGTCACTCGGCCACGTCACAGGGGAACGTGGACTTGCACTTGCA 2038
                                                                                                                       2039 GCAGTCAACTGGAATGGACAATTTCAAGCCTCCTGAGGTTCAGGCGGCATAATCCTCACT 2098
                                                                                                                                                                                                                                                                                                                                                                                                                                        1919 AAGAAGCAGCTGAGCCTCCTCCCCAGGCCCGAGGGGTGAGGAGTGACAGGCGAGACGGA 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1859 CATGTTAACCTCACCCTACAGATGAAGATAATAGAGCAGGAAAGAGAAATCGAGGAACTC 1918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1775 GTCCAGCTGCTGACCAGG------ 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1667 -----TTCCAGCCCTTCGGGACAGAGATGGAGCGG---GCAGAGGTCCTGACGGGC 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1607 GGATCGGAGTATGATGCCAAGTCAGACATGTACAGCGTCGGCGTGATCCTGCTGGAGCTC 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1547 GCACCCACACACTTCCCGAGTGGGCACCTGTCTGTACGCCTCGCCCGAGCAGTTGGAA 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1487 CTGGCCTGCGCCGACATCATCCAGAAGAATGCGGCCCGGACCAGCAGAAACGGGGAGAGA 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1427 AAGCCTAGAAATATTTTTCTTCATGGTCCTGATCAACAAGTGAAAATAGGAGACTTTGGT 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1715 GTGCGAGCTGGCCGCATACCCGACTCCCTCAGTAAGAGGTGCCCGGCGCAGGCCAAGTAC 1774
                                                                                                                                                                                             199 SerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGlyGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ProSerThrValGlyAlaGluAlaGlnGluGluPheLeuArg------ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 TyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSerTyr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 ArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSerGly 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 ArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGluThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 GluAspTyrPheProSerValProAsp-----AsnAlaGluLeuValLeuLeuThrLeu 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 LeuProGluArgGlySerArgLeu-----CysLeuTyrGluAspGlyThrGluLeuThr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 ProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGln 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPhe------Gln 38
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7729-7733
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Cloning of the cDNA of the heme-
regulated eukaryotic initiation factor
2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
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-----SerArgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPhe 230 :::|||:::
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GENERAL INFORMATION:
APPLICANT: Massac
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TITLE OF INVENTION: DNA E
TITLE OF INVENTION: Eukar
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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 NAME/KEY:
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CELL TYPE:
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Cloning of the CDNA of the heme-regulated eukaryotic initiation factor 2alpha (eIF-2alpha)kinase of rabbit reticulocytes:
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TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-069-023-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vequence 21, Application US/09069023A Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -748-451-2 (1-338) x US-09-069-023-21 (1-2143)
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105 GlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHis 124
                                                                                                                                    389 ATCCACCTGGACTCCGACGGCACGGAGATCGATGATGAGGAGTACTTTCGCACCCTCGAC 448
                                                                                                                                                                                                                                                                                                                   329 CTGGAGGAGATCCGCAGCAAGGTGGCGGAGAAGTTCGAGAAGTGCGACCACCTGCCCACC 381
                                                                                                                                                                                                                                                                                                                                                                                                      269 AAGCCTTTCAAAGTCAAGGACGTAACACGCAACATTAAGAAGGCTGTCTGCGCCTCCAGT 328
                                                                                        85 IleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAlaGln 104
                                                                                                                                                                                 65 AspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAsp 84
                                                                                                                                                                                                                                                                    46 LeuCysLeuTyrGluAspGlyThrGluLeu---ThrGluAspTyrPheProSerValPro 64
                                                                                                                                                                                                                                                                                                                                                            26 CysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGlySerArg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGlyArgSer 25
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 198-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 1167
TYPE: DNA
ORGANIZM; MUS musculus
US-09-069-023-19
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US-09-069-023-19
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                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-748-451-2 (1-338) x US-09-069-023-19 (1-1167)
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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09069023A Patent No. 6348573
                                                                                                                                                            No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 LeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIle 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 TACGTGACGAT-AACCACTCCACATGGCAACGAGGCAGGAAC-----TGGAAACGGAGA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 AsnValSerGlnAsnIleAlaAlaGluThrArgAlaGluAspProProTrpPheGluGly 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 ---PheThrSerGluAsnLeuLysLeuValHisIleVal---CysHisLysLysThrThr 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709 CAACTCGTTGGTGGACATCACGGGAAAGGAGTTTATGGAGCAGCTCAAGGATGCGGGAAG 768
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Matches:
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RESULT 11
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                ATTORNEY AGENT INFORMATION:
NAME: LAISON, MAITHA T.
REGISTRATION UNDER: 3238
REFERENCE/DOCKET NUMBER: UBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEPAX: (970) 668-2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                   SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                            CITY: Frisco
STATE: CO
                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: WORDER
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCTGGAGACCTTGCTGCTACGTGGAGTGCTAACACTGGTCCTGGAGGAGGATGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GlnAsnIle-AlaAlaGluThrArgAlaGluAspProPro---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCCAAAACACAGCAAGGACATCGCCCGCATCACCTTCGATGTGTACAAGCAAAATCCC 546
        FOR
                                                                                                                                                                                                                                                                                                                                               E: Oppedahl
PO Box 5270
                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalchman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chopra, Vikramjit Singh
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Huq, A.H.M. Mahbubul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayden. Michael R.
                                                                                                                                                                                                                              IBM Compatible
     ID NO:
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DB:
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Best Local Similarity:
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OTHER INFORMATION:
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ProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIle
                                                                                                                                                                                                                                                                                              ACACAGATCGCCGAG---
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                                                              TrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsn
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Mismatches: Indels:	Percent Similarity: 36.18% Conservative: 49	702-3 Scores:	; NAME/KEY: CDS : LOCATION: 113 1105	DEDNESS:	; SEQUENCE CHARACTERISTICS; ; LENGTH: 1689 base pairs ; TYPE: nucleic acid	; TELEFAX: (512)474-7577 ; INFORMATION FOR SEQ ID NO: 3:	; REFERENCE/DOCKET NUMBER: UTSD:546 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (512)418-3000	ATTORNEY, AGENT INFORMATION: NAME: McMillian, Nabeela R. REGISTRATION NUMBER: P-43,363	APPLICATION NUMBER: US/09/061,702 FILING DATE: Concurrently Herewith CLASSIFICATION:	; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible	: COUNTRY: USA : ZIP: 77210-4433	CITY: Houston STATE: TX	Д. H.	; APPLICANT: Wang, Xiaodong ; APPLICANT: Liu, Xuesong ; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN ; TITLE OF INVENTION: APOPTOSIS	pplicati 65737 RMATION:		QY 332 nProValArgLysArgGln 338	1250 TTGACCGGTGACACTGTCATCCAGGGGAGTGCCACCAGGCCTCCGGGGCCCCACCGGAGCCA 1309	1190 TATECTGGCCCAGAAGATATTAGTGAGCTTCTGCACTCGATCACCCTGCTTGCCCAC	Db 1187 CAG 1189 Oy 303 HisileValCysHisLysLysThrThrHisLysLeuAsn-CysAspPro 318	Oy 283 GluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeuLysLeuVal 302	GluLysLysArgThrIleIleProThrLeuValGluAlaIleLysGluGlnAspGlyArg	Db 1082CTTGAGGAACCCACCCTCATCAGCTGTGCAGGATCCACAGATCACCTTCTC 1132
	yo da	Db 43	0 8	P 04	Db .	Qy	Db Db	g g		Qγ	DЪ	Db		Оy	Qy Db	Qy Db	Db .	Qy	Db Qy	Оу	Qy Db	Db	Qy	DB:
8 LeulysArqlysGlnProValArqlysArqGln 338	308 LysLysThrThrHisLysLeuAsnCysAspProSerArgIleTyrLysProGlnThrArg 327	869	שנייים בייים של זויסים בייים של זויסים בייים בייים בייים בייים בייים בייים בייים בייים בייים בייים בייים בייים	8 IleīleProThrLeuValGluAlaīleLysGluGlnAspGlyArgGluValAspTrpGlu	:::	8 GluSerArgIleLeuPheSerThrTrpAsnLeuAspHisIleIleGluLysLysArgThr	232MetAspSerCysLeuSerArgHisSerIleAsnProTyrSerAsnArg 247 132	716 GAGGCAGCCTCTTGTCAAAGCAGGAAGAGTCCAAAGCTGCCTTTGGTGAG 766	6 AGAGAGGAAGTGCGTCAGTCCAAGCAGCTCCTGCAGCTGTACCTCCAGGCTTTTGGAGAAA	193 MetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLys 212	1/3 SETTYPTOSETTNYALGLYALAGLICLUGLUPHELEUARGVALLEUGLYSET 192 193 CAGAGTTGTGCCACCGTCCAGCGGCTGCAGCACACACTCCAACAGGTGCTTGACCAA 655	9 GAGGAGGACCTCCAGATGCTTGACGCTCCCTGCTCAGACCTGGCTCAGGAACTACGT	153 SerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSer 172	133 GluThrArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLys 152	113 ProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerglnAsnIleAlaAla 132	93 HisGluProGlnValGlyLeurleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAla 112 ::: ::: ::::::::::::::::::::::::	377 GCTAGTAATGAGAAATGGGCATAC 400		54 GluLeuThrGluAspTyrPheProSerValProAspAsnAlaGluLeuValLeuLeu 72 .::: ::: 317 ATAGTGGATGACGATTACTTTCTGTGTCTTACCTTCCAATACTTAGTTTTCTGCATTC 376	35LeuargPheGlnLeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThr 53	17 ArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCys 34 :::	140 CCAGAATCTGGCGAGATCCGGACTCTAAAGCCGTGTCTGCTGCGCCGCAACTACAGCCGC 199	σ μ	, ,

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                                    GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM 03333
                                                                                                                                                                      Sequence 13, Application US/09069023A Patent No. 6348573
     CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27
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Local Similarity:
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APPLICATION NUMBER: US
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                      RESULT 15
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Pred. No.:
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                                                                                                                              Sequence 1, Application US/08794158 Patent No. 6387655
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SOFTWARE: PatentIn Ver
SEQ ID NO 13
                                                                                                              GENERAL INFORMATION:
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                 APPLICANT: Burnett Jr., J. I
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
TITLE OF INVENTION: Excitati
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 NUMBER OF
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and Related
                 Excitatory Amino Acid Receptor Protein and Related Nucleic Acid Compounds
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US-09-748-451-2 (1-338) x US-08-794-158-1 (1-2637)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Indianapolis
STATE: Indiana
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                                         146 uSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSe 166
                                                                                                                                                                                      605 CTGAGATCTTGCGCTTCTTCAACTGGACCTACGTGTCCACAGTAGCCTCCGAGGGTGATT 664
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T---CGCTACGGCGGAGAAGGTGGGCCGCTCCAACATCCGCAAGTCCTACGACAGCGTGA 778
                                                                                           ACGGGGAGACAGGGATCGAGGCCTTCGAGCAGGAAGCCCGCCT---GCGCAACATCTGCA 721
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US-08-794-158-3
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                                                                                                      COUNTRY: U.S.

ZIP: 46285

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/794,158

FILING DATE:

CLASSIFICATION: 435

APTODENCY ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08794158 Patent No. 6387655
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APPLICANT:
APPLICANT:
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APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
TITLE OF INVENTION: Excitatory Amino Acid Receptor Protein
TITLE OF INVENTION: and Related Nucleic Acid Compounds
NUMBER OF SEQUENCES: 3
                                                               NAME: Webster, Thomas D.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                   NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,872 REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1154 AGCAAGAGTCCAAGATCATGTTTGTGGTGAACGCGGTGTÄTGCCATGGCCCACGCTTTGC 1213
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SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                              US-09-748-451-2 (1-338) x US-08-537-342-1 (1-4322)
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                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 02-OCT-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pedersen, Olu
APPLICANT: Bjorbaek, Chr
APPLICANT: Hansen, Lars
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                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                             TYPE: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Agris, Dr. Cheryl H. REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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1364 CCCTCTTCAGATCAACTAATGGCAGGAAACCTTAATAAAAAACAT---GAAGGAGGAGCT 1420
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                                ProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGlyArg 24
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Bjorbaek, Christian
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1958 CAAAGTTGGAATGTTCTGGAAAGTCAGGGAAAATCAAGAGAGAATAAGACAAACATAACA 2017
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                                                                                                                                                                                                                                                                                                                                                                                                       2198 AAGACAACATCAGAAAGTACTCCAGAAAGCATGTCTGCTAGAGAAAAAAGCAATAATTGCT 2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1937 GAT-----AATAGCCCACAGCATAAA 1957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1760 AATTTAAGTTGGGAA----GAAGCTGTGTTAACCCCAGAGCATCATCATTTGACTAGTGAA 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 GAACATACCGCAATCCCCACCCGGGCAATCACAGCAGATGTGTCTCATTCACCAAGGACA 1759
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                                       2357 CTTTGTCAACGAGATACAGTAGGTGTAATCTATGACAATGATTTTGAAAAGGAATCACGT 2416
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                                                                           289 ------PheTyrGlyLeuLeuPheThrSerGluAsnLeuLysLeuValHis 303
                                                                                                                                                                                                                   270 ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAspTrpGluTyr--- 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 --- ArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 PheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIle------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 SerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGlySer
                                                                                                                                                              --------GCGTTTGATCCACATGAAGGGAGAAATGATGATTCACATTATACC 2356
                                                                                                                                                                                                                                                                                                                                          -----SerThrTrpAsnLeuAspHisIleIleGluLysLysArgThrIleIle 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AsnProTyrSerAsnArgGluSerArgIleLeuPhe 253
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SEQ ID NO 17
LENGTH: 1114
TYPE: DNA
ORGANISM: Mus musculus
US-09-069-023-17
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US-09-069-023-17
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Best Local Similarity:
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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Inohara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
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                                                                                         741 TATGTCCTATGCTGCACAGATGACGGGACAGTTCCTGGTCTA------
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152 LysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluVal 171
                                                                                                                                                      135 Arg-----AlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSer 151
                                                                                                                                                                                                                681 GGTGTCCTACGACATCCGATGCACCAGGTTCAAGGCCGTGTTAAGGAATCTGCTGAGGTT 740
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                                                                                                                                                                                                                                                                                                                                          636 CCTCGGCTGTCTCAA-----TGT-----CAAAGCCACGATGTACGAGATGTACTC
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; OTHER INFORMATION:
US-09-103-840A-2
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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  TTAGCGTTGACCAAT
                                                                                                              TTGTCGTTG-----ATAAGGTTTTGCACCTGGGCCGAGAAAGCGGAGATG-----
                                                                                                                                                                       ---TCGGTGAGGATGCGCAGCTGCTCGAGCACA-----TGGTTCAGGTTCGGG
                          LeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAla 91
                                                        ---TTCCCCAGCAGGGCGTCGACCGCGCGCGCGCGCTCGTTGAACGCGGCGATCAGGGTC
                                                                                    TyrPheProSerValProAsp-
                                                                                                                                                                                          PheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGln 38
                                                                                                                                                                                                                                                        LeuGlnLysProLysSerValLysLeuArgAla-----LeuArgSerProArgLys 18
                                                                                                                                           LeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GCAGCCATCCCCCAAGCCTAGCACCAAAGGCTGGTTCATGTAACCAGG 872
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US-09-748-451-2 (1-338) x US-09-103-840A-1 (1-4411529)
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 1, Application Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRA
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24256-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FLEISCHMAN, Robert APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4411529
TYPE: DNA
201801 CTGAATCTGCCCAAGATCGTCAGGGTTTCAGCCAAATCCTCCTTGCGGTCGACCAACAGG
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                                          LeuGlnLysProLysSerValLysLeuArgAla-----LeuArgSerProArgLys 18
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	Db 20	Qy . 20	Qy .	Qу Db 20	Оу рь 20	Qу Db 20	Qy Db 20	Оу Db 20	Db 20	Qу 2(Qу Db 20	Qу Db 2(Qу Db 2(
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•	sp 233 201161	yGlySerArgLeuCysThrProGluGlyTrpPheSerCysGln-GlyProPheAspMetA 233 	tCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGl 213 ::::: :::	rValGlyAlaGluAlaGlnGluGluPheLeuArgValLeuGlySerMe 193	<pre>gTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSerTyrProSerTh 177 </pre>	AspProProTrpPheGluGlyLeu-GluSerArgPheGlnSerLysSerGlyTyrLeuAr 157	AsnIlealaalaGluThrArgAlaGlu 137	AspGluGlnAlaProGlnArgClnArgLeuLeuAlaAspLeuLeuHisAsnValSerGln 128 ::: TCGTCGCGCTTGCCGATG	PheHisGluProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCys 108 ::::: ::::::	LeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSerAspIleArgArgPheLeuSerAla 91	TyrPheProSerValProAsp	LeuProGluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAsp 58	PheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGln 38
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Search completed: May 26, 2003, 17:28:0 Job time: 2100 secs

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Command line parameters:

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-OP-CGR2_1/USPFO_Spool_US09748451/runat_21052003_153830_16347/app_query.fasta_1.519
-DB-Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -TRHE_MAX=100
-THR_MIN=0 -ALIGN=20 -MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE-500 -MINLEN=0
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-NCPU-6 -LOCPU-3 -LOC_MAP -LARGEDUERY -NGCNES=0 -WAIT -DSSPLOCK-100
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-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           Query
Score Match Length DB ID
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           1789 100.0
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102.5 5.7
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11: //cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12: //cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

13: //cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

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1789
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                                    LeuValHisIleValCysHisLysLysThrThrHisLysLeuAsnCysAspProSerArg
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TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN
FILE REFERENCE: 15966-521 NIK1 protein complexes
CURRENT APPLICATION NUMBER: US/10/242,943
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US/09/167,206
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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US-09-748-451-2 (1-338) x US-10-161-803-29 (1-1862) QY 4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23	Percent Similarity: 34.42% Conservative: 50 Best Local Similarity: 20.87% Mismatches: 128 Query Match: 5.73% Indels: 115 DB: 9 Gaps: 16	0.00583 Length: 102.50 Matches:	; ORGANISM: Homo sapiens US-10-161-803-29	; SOPTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 29 ; LENGTH: 1862 ; TYPE: DNA	ILING DATE: 2002-06-03 LICATION NUMBER: US 60/295,264 ING DATE: 2001-06-01 SEQ ID NOS: 61	THE OF INVENTION: TREATMENT OF INSULIN RESISTANCE AND RELATED CONDITIONS THE REFERENCE: 421452000300 CURRENT APPLICATION NUMBER: US/10/161,803	OR DIAGNOSIS AN	; Sequence 29, Application US/10161803 ; Publication No. US20030092028A1 ; GENERAL INFORMATION: ; APPLICANT: Ma, Yuanhong	RESULT 3 US-10-161-803-29	1484 GAATAAAAAAGAAATCCATATCTTA	- 1	Qy 286TrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerGl 297	Db 1370CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG 1423	Qy 270 ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp 285	Qy 256TransnleursphisileIleglulyslysarghrileile 269 1	GAAGGCGAGGAGAACATTCTCTGCCTCTTCCAAACTTTTCCTCCTGAACCTG		Oy 224 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243 ::: ::: :::::::::::::::::::::::::::::	Db 1196GACCTG 1201	Qy 204 GlySerTyrPheAspArgGlyAlaLysGlyGlySerArgLeuCysThrProGluGlyTrp 223	1142	rAsn	Qy .166SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183 . ::::::
рр 1505 Оу 297 рр 1565			Qy 256 Db 1394	Qy 244 Db 1337	Oy 224 Db 1283	Db 1277	Оу 184 Db 1223 Qу 204	•	_L		Qy 144	Db 986	0у 139		Db 869 Qy 119	Qy 104	m	рь 752 Qy 84	ОУ 64	Db 696	Qу 44	6	Db 627 Qy 24
	CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAGTrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerGl ::::::	ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp	6TrpAsnLeuAspHisIleIleGluLysLysArgThrIleIle 269		4 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243 ::: :: :::::		4 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203				GlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyr		ProProTr		ATTCAGGAACAGCATGTC		:::		4 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83	6AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 751		HII::: II:::	

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Best Local Similarity:
Query Match:
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SEQ ID NO 43
LENGTH: 1864
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
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TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
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THER INFORMATION: Incyte ID No. US20020156263A1 127987.19
5-974-298-43
    1121 TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG 1180
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                                                                                                                                                                                                                                             CTGCGTGACGTACGTCAGCAATAT---GAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCA 1000
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                                                                                  GCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACC 1120
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24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43
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yte ID No.
580 GAATAAAAAAAATCAAT 090-793 090-793 100. US20020137081A1 1NFORMATION: SERENCE: PA-0028 US FERENCE: PA-0028 US FERENCE: PA-0028 US APPLICATION UMBER: US APPLICATION UMBER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION UNDER: US APPLICATION US APPLICATION US BURNATION: Incyte ID 090-793
SULT 5 -10-044-090-793 Sequence 793, Application US/10044090 Patent No. US20020137081A1 GENERAL INFORMATION: APPLICATIO: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVAT FILE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVAT CURRENT FILING DATE: 2002-01-09 NUMBER OF SEQ ID NOS: 850 SOFTWARE: PERL PROGRAM SEQ ID NO 793 LENGTH: 1892 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID NO. US20020137081A1 2812002CB1 -10-044-090-793

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US-09-974-298-44
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714 AGAAATTGCAGG---
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NAME/KEY: mlsc_feature
NOTHER INFORMATION: Incyte ID No. US20020156263A1 1397781.7
US-09-974-298-44
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CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 44
LENGTH: 3405
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ORGANISM: Homo sapiens
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-----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
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                                                                                                                                  -----SerCysGluSerArgIleArg----- 165
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEO ID NOS: 194
SOFTWARE: PERL Program
SEO ID NO 36
LENGTH: 3405
TYPE: DNA
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APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David
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TITLE OF INVENTION: GENES EXPRESSED
FILE REFERENCE: PA-0038 US
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Sequence 101, Application US/10043487 Publication No. US20030055220A1
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                                                                                                                                                                                                                                               -----CTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTCAG 166:
                                                                                                                                                                                                                                                                                   ProThrLeuValGluAlaIleLysGluGlnAspGlyArgGluValAsp-----
                                                                                                                                                                                                                                                                                                                                                ----TrpAsnLeuAspHisIle------
                                                                                                                                                                                                                                                                                                                                                                                                 ---GAAGGCGAGGAGCAGGATTTCTCTGCCTCTTCCAAACTTTTCCTCCTGAACCTG
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                                                                                                                                                                                                          -----TrpGluTyrPheTyrGlyLeuLeuPhe-ThrSerGl
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SEQ ID NO 101
LENGTH: 1218
TYPE: DNA
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APPLICANT: HYBRIGINICS
APPLICANT: PIETE, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypepti
TITLE OF INVENTION: mammalian polypeptides
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PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
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CURRENT FILING DATE: 2002-04-30
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)-043-487-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
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                                                                                                                                                                                                                                                                                                                     679 GAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGAC 738
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184 GluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgSerMetGlnTyrAsn 203
                                               859 GAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAGACACTATTGGC----CGCCTGCAG
                                                                                                                                     799 TGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATG 858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43
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                                                                                         ----SerTyrLeuArgGluValSerSerTyrProSerThrValGlyAlaGluAlaGln 183
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Best Local Similarity:
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SEQ ID NO 30
LENGTH: 220
TYPE: DNA
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APPLICANT: Che
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CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION UMBER: US 60/295,264
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS AND RELATED CONDITIONS
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  710 GTTGACAATGCGTCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAA 769
                                                                                      654 ---AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 709
                                                                                                                                                                                                                                                                        585 AAGCCCGCGTCG---AGGTGGAGCGCGACAACCTTGGCCGAGGACATCATGCGCCTCCGGG
                                  64 ProAspAsnAlaGluLeuValLeuTeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83
                                                                                                                                   44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63
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                                                                          GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUD
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOIL03
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
LENGTH: 69327
                                                                                                                                                                                                                                      Sequence 3, Application US/09777921A Patent No. US20020115136A1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m1sc_feature
; LOCATION: (1)...(69327)
; OTHER INFORMATION: n - A
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Query Match:
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                                  gLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLe 236
                                                                        AGTGCTTAACTTGGAAAGGAACAATCAGTAC----CAGCCGCTGCAAAATCATGCCAA
                                                                                                              gLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLysGlyGlySerAr
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                                                                                                                                                                                                                                                                                                                                                -GluSerArgPheGlnSerLysSerGlyTyr-----LeuArgTyrSerCysGluSe 162
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Query Match:
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; ORGANISM: Homo sapiens
US-09-923-779-149
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CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 1749
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APPLICANT: Xu, Jiangchun
APPLICANT: Kalos, Michael D.
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                                                                                                                                                                                                                                            851 AAAAATTGCAGG------
                                                                                                                                                                                                                                                                                                                                        794 AAGCCCGCGTCG---AGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGG
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                                                  919 GTTGACAATGCGTCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAA 978
                                                                                                                                              863 --- AGGAGATGCTTCAGAGAGAG-GAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAT 91
                                                                                                                                                                                          44 SerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPheProSerVal 63
                                                                                                                                                                                                                                                                                         24 ArgSerCysGlnGluValLeuArgLysGlyCysLeuArgPheGlnLeuProGluArgGly 43
                                                                                              64 ProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGlyTyrValSer 83
                                                                                                                                                                                                                                                                                                                                                                                     4 LysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGly 23
  AspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGlnAlaAla 103
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97.50
34.23%
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                                                    PRIOR APPLICATION NUMBER: 2002-01-30
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3:1
SEQ ID NO 7
SEQ ID NO 7
LENGTH: 2673
PUBB: DNA ORGANISM: Rattus norvegicus
US-10-060-425-7
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US-10-060-425-7/c
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APPLICANT: Hiebsch, ronald
TITLE OF INVENTION: Methods of Assessing Wolframin Protein Activity
FILE.REFERENCE: 00450.US1
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10060425
Patent No. US20020164650A1
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/060,425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1036 ATTCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCC 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 PheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHisSerIleAsnPro 243
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  0.0623
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202	1	Db 1953 GAACCAGCAAAAGAGCAGGATGGCCGTGAGCCACCAGAATGAGCTTCACTATGGAGCT 1894	Qy 274 GluAlaIleLysGluGlnAspGlyArgGluValAspTrpGluTyrPheTyrGly-Le 292	Db 1995 TGTGGAATTGTAGACCTTCATGCCTTCCGACCGGTACACGTA 1954	Qy 255 hrTrpAsn-LeuAspHisIleIleGluLysLysArgThrIleIleProThrLeuVal 273	Db 2041TCCAGGCCCGTGGCCCACACAGGAAGCCATATTGCTGCCAGGTGAG 1996	Qy 236 euSerArgHisSerIleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerT 255	Db 2077TGCACAGGATCTGGGTCCGGGCCATGTTAGTCTCCT 2042	Qy 216 rgLeuCysThrProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysL 236	199 erMetGlnTyrAsnGlySerTyrPheAspArgGyAlaLysGlyGlySerA 216 :::	GATGGCCGACTCGGCGCTGTTGTCGATCTCGGT	Oy 181GluAlaGlnGluGluPheLeuArgValLeuGlySerMetCysGlnArgLeuArgS 199	Db 2214 ACCGTACAGGCAGCGCATCCAGTCACCCAGGAAGAACGGGAGCATGTT 2167	Qy 162 erArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGlyAla 180	Db 2248ACGTGTTACCAGAGCTACAGGATGGGTAGGCCTC 2215	Qy 142 heGluGlyLeuGluSerArgPheGlnSerLysSerGlyTyrLeuArgTyrSerCysGluS 162	Db 2307 GATGTGGCAGGGGTGCTTGGCCAGCTGCTTGAGACGGCAGAGCTCCTCCTCAGCCGTGG- 2249	ValSerGlnAsnIleAlaAlaGluThr	N	יינים ומיים ליינים ליי	Qy 85 ILEATGATGPheLeuSerAlaPheHlsGluProGlnValGlyLeuIleGlnAlaAlaGln 104 :::: :::::: Db 2391 GTCGTCTTCGTGGCCGCGGTT	. 2451	Qy 76 GlnAlaTrpGlnGlyTyrValSerAsp 84	 56 ThrGluAspTyrPheProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGly 75	Db 2562 CAGCTGTGTCATGCAATTGAGGCAGCTGATGGCCTTGAGCTCGAAGACGGGCCACTTGCT 2503	Qy 45 ArgLeuCysLeuTyrGluAspGlyThrGluLeu 55	Db 2615TGCACCGTGCTACGCCAGTCCTGTTCGATCTTTAC-GTGCCTCCGGGCAGGGGA 2563	GlyCysLeuArgPheGlnL	AAC	Qy 6 LysSerValLysLeuArgAlaLeuArgSerProArgLysPheGlyValAlaGlyArg 24	US-09-748-451-2 (1-338) x US-10-060-425-7 (1-2673)	5.39% Indels: 9 Gaps:	Score: 96.50 Matches: 106 Percent Similarity: 35.44% Conservative: 34 Best Local Similarity: 26.84% Mismatches: 125
-																	.3	\ \ \ •						 •	•					•			•
	Db 1361AG	75 G1y	1325	י ט ני	1283		1.4/	1247	US-09-748-451-2 (1-	Query Match: DB:	Percent Similarity: Best Local Similari	Pred No.:	NS-09-995-898A-32	; LOCATION: (123)		; FEATURE: ; OTHER INFORMATI	<pre>; TYPE: DNA ; ORGANISM: Artif</pre>	; SEQ ID NO 32 ; LENGTH: 1922		PRIOR APPLICATIO	; CURRENT FILING D ; PRIOR APPLICATIO : PRIOR FILING DAT	; FILE REFERENCE:	; APPLICANI: WILL ; MITLE OF INVENTI	9	; Sequence 32, Appl ; Publication No. U	A868		1712		1773	210	304	Db 1893 CCGAG

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I 02 '	NUMBLER OF SEQ ID NOS: 50 SOPTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 32 LENGTH: 1922 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: MBP-human zcytoR19 fusion protein polynucleotide OTHER INFORMATION: sequence FEATURE: NAME/KEF: CDS LOCATION: (123)(1922) -09-995-898A-32 ignment Scores: ed. No.: 0.0503 ignment Scores: 95.50 rcent Similarity: 34.29% rcent Similarity: 34.29% ST Local Similarity: 24.49% ETY Match: 5.34% igns: 101 Gaps: 12 -09-748-451-2 (1-338) x US-09-995-898A-32 (1-1922)	NUMBLE OF SEQ ID NOS: 50 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 32 LENGTH: 1922 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: MBP-human zcytoR19 fusion protein polynucleot OTHER INFORMATION: sequence FEATURE: NAME/KEF: CDS LOCATION: (123)(1922) -09-995-898A-32 ignment Scores: ed. No.: 95.50 rcent Similarity: 34.29% st Local Similarity: 34.29% st Local Similarity: 5.34% st Local Similarity: 5.34% st Local Similarity: 5.34% st Local Similarity: 9.34 Nismatches: 101 sery Match: 9 15 SerProArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLys
	ignment Scores: 0.0503 Length: 1922 ed. No.: 95.50 Matches: 60 ore: 95.50 Matches: 24 reent Similarity: 34.29% Conservative: 24 st Local Similarity: 24.49% Mismatches: 101 st Local Similarity: 24.49% Mismatches: 100 ery Match: 5.34% Indels: 60 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 12 caps: 13 caps: 14 caps: 16 caps: 17 caps: 17 caps: 18 cap	gnment Scores: 0.0503 Length: 1922 d. No.: 95.50 Matches: 60 re: 95.50 Matches: 24 cent Similarity: 24.49% Mismatches: 101 t Local Similarity: 24.9% Mismatches: 101 ry Match: 5.34% Indels: 60 gaps: 12 09-748-451-2 (1-338) x US-09-995-8988-32 (1-1922) 15 SerProArgLysPheGlyValAlaGlyArgSerCysGlnGluValLeuArgLysGlyCys 114

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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(87)
US-09-216-393-282
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Best Local Similarity:
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UTRENT FILING DATE: 1998-12-18
ARLIER APPLICATION NUMBER: 08/994,825
ARLIER FILING DATE: 1997-12-19
ARLIER OF SEQ ID NOS: 364
SOFTWARE: PATCHINI Ver. 2.0
SEQ ID NO 282
LENGTH: 1225
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CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 284
LENGTH: 1225
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Patent No. US20010014447A1
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                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo US-09-764-891-5984
                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5984, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir FILE REPERRENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pat
SEQ ID NO 5984
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TYPE: DNA
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               IleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeu
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RESULT 17
US-09-764-891-5985/c
US-09-764-891-5985, Application US/09764891
Publication No. US20030077808A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5985
LENGTH: 1282
TYPE: DNA
ORGANIZM: Homo sapiens
US-09-764-891-5985
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                                                         US-09-748-451-2 (1-338) x US-09-764-891-5985 (1-1282)
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Best Local Similarity:
                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                          Alignment Scores:
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CURRENT FILING DATE: 2001-01-17
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ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
'ILE REFERENCE: PC006
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APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Both, Andrew
APPLICANT: Both, Andrew
APPLICANT: Van Huffel, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREV
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 1006-04-14
NUMBER: 1016
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US-09-834-975-958/c
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                                               SEQ ID NO 958
LENGTH: 4967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                               SOFTWARE:
TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 19
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APPLICATION NUMBER: 60/241,809
STITING DATE: 2000-10-20
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FILING DATE: 2000-08-14
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
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FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/228,924
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APPLICATION NUMBER: 60/234,274
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FILING DATE: 2000-07-26
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APPLICATION NUMBER: 60/180,628
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OF INVENTION: Nucleic Acids, Proteins,
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APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: 6
FILING DATE: 2000-09APPLICATION NUMBER: 6

2000-09

60/229,344

60/234,997

ION NUMBER: 2000-09-01

60/229,345 60/229,343

R APPLICATION NUMBER: 60/2

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60/229,513 60/229,287

APPLICATION NUMBER: 60/231,413 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/229,509

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                                                                                                                                                                                                                                                           Query Match:
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PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-11-17
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DR FILING DATE: 2000-10-20

DR APPLICATION NUMBER: 60/22

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DR FILING DATE: 2000-09-14
DR APPLICATION NUMBER: 60/23
DR FILING DATE: 2000-09-08
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APPLICATION NUMBER: 60/249,211
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APPLICATION NUMBER: 60/249,217
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/231,244
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,064
                                                                                                                                   APPLICATION NUMBER:
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                                                                    6204 CAGCTGGAGAACCCCCTGGCC-
                            134 ThrArgAlaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSer 153
                                                                                           114 GlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGlu 133
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CCCATGTCACAGACAGAAGGGCATTGGGAGGGAAATGGAAAAGCGATTAGAGTCCAGTTAT 610:
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                                                                    ---TGTGGGAACGTAGTCAGGGAA 6163
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DR PELLING DATE: 2000-09-05
DR APPLICATION NUMBER: 60/236,367
DR APPLICATION NUMBER: 60/237,039
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DR APPLICATION NUMBER: 60/236,370
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DR APPLICATION NUMBER: 60/237,037
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DR APPLICATION NUMBER: 60/237,040
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APPLICATION NUMBER: 60/249,218
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,213
FILING DATE: 2000-11-17
FILING DATE: 2000-11-17
FILING DATE: 2000-11-17

APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17

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SOFTWARE: PATENTIN Ver. 2
SEQ ID NO 9340
LENGTH: 11598
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-891-9340/c
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NERAL INFORMATION:
PPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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CURRENT FILING DATE: 2001-01-17
     5943
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                                                                                                                                                  6042 --- CCATCTACTGCTGGACCAGCAGGGCACGTTCTCTCCAGGCTTCACCCACTGGGGAGC
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                                                                         5985 CTTTGT-----ACATTGCAAAGTGGAACCAAGTCATGGGATGAA-----CAG
                                                                                                                                                                                                                             6102 ACTGCGATTGTTTCATGGGAACCACTAGGTGTGCCAGCACCAGGCCCAGAGTGAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                  6204 CAGCTGGAGAACCCCCTGGCC------TGTGGGAACGTAGTCAGGGAA 6163
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6264 GAACCACAGGCAGGCCCGGTGACCACAGGGATACTTGTCTTGGTGTGCTCCCCTAGCCAG 6205
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                                                                                                                                                                            174 TyrProSerThrValGlyAlaGluAlaGlnGlu---GluPheLeuArgValLeuGlySer 192
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                                                                                                                                                                                                                                                                 154 GlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuArgGluValSerSer 173
                                                                                                                                                                                                                                                                                                                                            134 ThrargalaGluAspProProTrpPheGluGlyLeuGluSerArgPheGlnSerLysSer 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 TyrProSerThrValGlyAlaGluAlaGlnGlu---GluPheLeuArgValLeuGlySer 192
                                   213 GlyGlySerArgLeuCysThrProGluGlyTrp 223
                                                                                                                                                                                                                                                                                                                                                                                                                      114 GlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsnValSerGlnAsnIleAlaAlaGlu 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 GluProGlnValGlyLeuIleGlnAlaAlaGlnGlnLeuLeuCysAspGluGlnAlaPro 113
GGTGGCCCAGAGTTAGCATTCCCAGAGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetCysGlnArgLeuArgSerMetGlnTyrAsnGlySerTyrPheAspArgGlyAlaLys 212
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cmrTGT-----ACATTGCAAAGTGGAACCAAGTCATGGGATGAA-----CAG 594.
                                                                                                                                                                                                                                                                                                         CCCATGTCACAGACAGAAGGGCATTGGGAAGAATGGAAAAAGCGATTAGAGTCCAGTTAT 610:
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Search completed: May 26, 2003, 16:58:10 Job time: 230 secs

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Title:
Perfect score:
Sequence:
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-MODEL-framet_D2n.model -DEV-xlh
-O_/cgn2_1/GSP0_spool/US09748451/runat_21052003_153830_16291/app_query.fasta_1.519
-O-/cgn2_1/USPP0_spool/US09748451_Tunat_21052003_153830_16291/app_query.fasta_1.519
-DB-EST -OFMT-fastap -SUFFIX-rist -MINNATCH-0.1 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MARITIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-20 -MODEL-LOCAL
-OUTFMT-pc -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09748451_eCGN_11_1906_etrunat_21052003_153830_16291 -NCDP-6 -ICPU-3.
-NO_MMAP -LARGEDUERY -NEG_SCORES-0 -MAIT -DSPBILOCK-100 -LONGLOG
-DEV_TIMEOUT=120 -MARKL_TIMEOUT=30 -THEADSIS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1789
1 MLQKPKSVKLRALRSPRKFG.....SRIYKPQTRLKRKQPVRKRQ 338
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em_estov:*
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 BQ715165
NIH-MGC http://mgc.nci.nlh.gov/. National Institutes of Health, Mammallan Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1014)		house mouse.	EST.	BQ715165.1 GI:21854064	BQ715165	AGENCOURT_8480637 NIH_MGC_129 Mus musculus	BQ715165 1014 bp mRNA linear EST 16-JUL-2002	

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Plate: LLAM13731 row: j column:
High quality sequence stop: 566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan,
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                                                     CysGluSerArgIleArgSerTyrLeuArgGluValSerSerTyrProSerThrValGly 179
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SerIleAsnProTyrSerAsnArgGluSerArgIleLeuPheSerThrTrpAsnLeuAsp 259
                                                                                                                                                                              ProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCysLeuSerArgHis 239
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/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
pcMv-SpORT6.1.ccdb; Site_1: EcoRv; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: th
is a NIH_MCC_Library."
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US-09-748-451-2 (1-338)
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Query Match:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Tissue Procurement: Lothar H
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Mammalia; 1
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Clone distribution: MGC clone distribution information can
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: Not1; Cloned unidirectionally. Primer: Oligo dy Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Grow and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5325440"
/clone_11b="NCI_CGAP_Mam4"
/tlssue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10830 row: a column: 05
                                                                                                                                                                                                                                 1 (bases 1 to 834)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 834)
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602796717F1 NCI_CGAP_Mam4 Mus
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                                                                                                                                                                                                tact: Robert Strausberg, Ph.D.
il: cgapbs-r@mail.nih.gov
                    quality sequence stop:
    Location/Qualifiers
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                    788.
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                                                             201 GlnTyrAsnGlySerTyrPheAspArgGlyAla---LysGlyGlySerArgLeuCysThr
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ProGlu-GlyTrpPheSerCysGlnGlyProPhe-AspMetAspSerCysLeuSerArgH
                                    CAGTACAATGGCAGCTATTTCGACAGAAGGTGCAGAAAGCCCCAGCAGCAGGCTCTGTACT
                                                                                                        GCAGCTCAAGAAGAGTACCTGCGAGTCCTTGGCTCCATGTGCCAGAAGCTCAAATCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4917772"
/clone_lib="NCI_CGAP_Mam4"
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Mismatches:
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High quality sequence stop: 685.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: LLAM11404 row: b column:
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                          ValAlaGlyArgSerCysGlnGluValLeuArg-LysGlyCysLeuArgPheGlnLeuPr 40
       GTGGCTGGCCGGAGCTGCCAGGAGGTGCTGCCAAGGGCTGTCTCCGCTTCCAGCTCCC
                                                                                               MetLeuGlnLysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPheGly
                                                                            ATGCTCCAGAAGCCCAAGAGCGTGAAGCTGCGGGCCCTGCGCAGCCCCGAGGAAGTTCGGC
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                                                                                                                                                                                                                                                                                                                                                                /lab_host="UHIUG"
/note="Organ: pooled colon, kidney, stomacn; vector.
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5162791"
/clone_lib="NIH_MGC_116"
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Note: this is a NIH_MGC Library."
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Plate: LLAM11513 row: p column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
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/note="Organ: pooled lung and spleen; Vector: pcMV-SPORT6 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size
                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:5204996"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
                                                                                                                                                                                      organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 855)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Capabs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                          BF165515
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://insge.lln.gov
plate: LLAM9270 row: j column: 04
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a 215 c 285 g 174 t 1 others
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/clone_llb="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic
Stem cell origin."
/lab_host="DH10B"
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/strain="CZECH II"
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Matches:
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BI916035/c
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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1 (bases 1 to 775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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                                rValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIleGl 101
                                                                                 SerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrp-GlnGlyTy 81
TGTGAGTGACAT-CGGTGCTTCCTCAGTGCTTTTCGCCAGCCGCACGCGTGGCTCATCCA
                                                                ProGluGlyTrpPheSerCysGlnGlyProPheAspMetAspSerCys
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                                                                                                                                                                                                                                                                                                                                                              full-length clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5248694"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                              (Invitrogen).
                                                                                                                                                                   1.28e-77
738.00
88.00%
81.00%
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                                                                                                                                                                                                                                                                                                            ning). Average insert size 1.7 kb, insert size range 1.5 kb. Library is normalized and enriched for 1.5 kb. clones and was constructed by C. Gruber ritrogen). Research Genetics tracking code 017..Note: is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BQ431184.1 GI:21170260
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
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AGENCOURT_7786920 NIH_MGC_92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health,
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/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:6068786"
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RESULT 9 BQ055307/C BQ055307 BQ055307 BQ055307 BQ055307 BQ055307 BQ065307 BQ065307 VERSION REYMORDS CST SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS NIH-MGC http://mgc.ncl.nih.gov/. BNALLOMAENT NATIONAL Institutes of Health, Mammalian Gene Collection (MGC) COMMENT COMMENT COMMENT Tissue Procurement: Lou Staudt CDNA Library Preparation: Rubin Laboratory	Qy 157 gTyr-serCysGluSerArg1leArgSer-TyrLenArg-GluValSerSerTyrPr 175 1111 ::: 1111 111 1111 11 1111 11	120 AlaAspLeuLeuHisAsnValSerGlnAsnIIeAla-AlaGluThrArgAlaGluAspPr	Oy 61 ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80 61 ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80 61 ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80 61 CCCAGTGTTCCCGACAACGCCGAGCTGGTGCTCACCTTGGGCCAGGCCTGGCAGGGC 551 Qy 81 TyrValSerAspIleArgArgPheLeuSerAla-PheHisGluProGlnValGlyLeuIl 100 61	21 ValàlaGlyArgSerCysGlnGluValLeuArgLysGlyCysLèuArgPheGlnLeuPro	US-09-748-451-2 (1-338) x BQ431184 (1-908) 1 MetLeuGlnLysProLysSerValLysLeuArgAlaLeuArgSerProArgLysPhegly 20	BASE COUNT 158 a 271 c 307 g 171 t 1 others ORIGIN Alignment Scores: 7.15e-75 Length: 908 Score: 716.00 Matches: 169 Percent Similarity: 87.31% Conservative: 3 Best Local Similarity: 87.79% Mismatches: 13 Query Match: 40.02% Indels: 12 DB: 14 Gaps: 2
Oy 149 eGInSerLysSerGlyTyrLeuArgTyrSerCysGluSerArgIleArgSerTyrLeuAr 169 :::	Oy 110 uGlnAla-ProGlnArgGlnArgLeuLleuAlaAspLeuLeuHisAsnValSerGlnAsnI 130	76 921 91 867	Alignment Scores: 1.61e-68 Length: 1071 Pred. No.: 664.00 Matches: 145 Score: 83.77% Matches: 15 Best Local Similarity: 75.23% Mismatches: 19 Query Match: 37.12% Indels: 13 DB: 14 Gaps: 2 US-09-748-451-2 (1-338) x BQ055307 (1-1071)	into ECORI/Xhol sites using the following 5° adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 248 a 344 c 278 g 201 t	/OU_XIEL="ICAXON:3000" /Clone=lib="NIH_MGC_99" /clone_lib="NIH_MGC_99" /tissuc_type="lymphoma, cell line" //tissuc_type="lymphoma, cell line" /lab_host="PH10B (phage-resistant)" /lab_host="PH10B (phage-resistant)" /lab_host="PH10B (phage-resistant) /note="Organ: lymph; Vector: pOTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: pOTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: /note="Organ: lymph; Vector: poTB7; Site_1: xhoI; Site_2: xho	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2049 row: o column: 16 High quality sequence stop: 595. FEATURES LCCation/Qualifiers source //db.w.ef="""-"

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Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html
Location/Qualifiers
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Buerstedde, J.M.
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                                                                        LeuLeuCysAspGluGlnAlaProGlnArgGlnArgLeuLeuAlaAspLeuLeuHisAsn
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                                                                                                                                                              CAGACGGAGCTGGTGCTGCGGCCCGGGGAGAGCTGGCCGGGC--
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/note="CB inbred strain"
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                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
cDNA Library Arrayed by: The I.M.A.G.E.
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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591 CCGTCCCTGACCCTCTGGCTTCCCAGGCTTA-AGGGAATTTCTCTGGCTCAGCTCCGGAA 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 ACAGAGGCAGAGGCTGTG-GCTGACCTCCTGCACAACGTCAGCAGAACA---TCGCGGGC 513
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URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Rawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and hayashizaki,Y.
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Computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa
K., Fikuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the
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81

US-09-748-451-2 (1-338) x BG705510 (1-716)

Query Match:

76.73% 70.30% 32.87% 12 1.12e-59 588.00

Gaps: Mismatches: Indels:

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                  Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                    Contact: Buerstedde JM
Cellular Immunology
                                                                        Gallus gallus bursal lymphocyte 
Unpublished (2002)
                                                                                                                  Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                               Buerstedde, J.M.
                                                                                                                                       Eukaryota; Metazoa;
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Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@Mfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No sl sequence available.
This clone (DKFZp66601116) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
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                                                                                                            TTCTCCTGCCAGGGTCCCTTTGACATGGACAGCTGCTTATCAAGACACTCCATCAACCCC
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cDNA-collection"
172 c 190 g 135 t
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                   498 GTGCTCCAGAAGCACAAGACTGTGAAGCTGCGGGCCCTGTGCAGCCCGAGGAAGTTTGGC
                                                                                                  61 ProSerValProAspAsnAlaGluLeuValLeuLeuThrLeuGlyGlnAlaTrpGlnGly 80
81 TyrValSerAspIleArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIle 100
                                                                                                                                                                                                                   41 GluargGlySerargLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe 60
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Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (lnfo@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
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RPCI-11-186H3.TV RPCI-11
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/db_xref="GDB:/571210"
/db_xxef="taxon:9606"
/clone="RPCI-11-186H3"
/clone=1b-"RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3124 row: D column: 06
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Seq primer: -21M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onpublished (2001)
Other_ESTs: H3124D06-3
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,T.S., Carter,M.G. and Ko,M.S.H.
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                                                          /note-"Vector: psport]; Site_1: Sall; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo coMA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb All
source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:H3124D06-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                              /clone="H3124D06"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Eutheria; Rodentia;
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e Set Mus musculus
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ORGANISM
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SOURCE

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US-09-748-451-2 (1-338) x BG086312
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                                                                                                        BI789500 537 bp mRNA linear LEST 12-MAR-2002 ic95e08.yl Melton Normalized Mixed Mouse Pancreas 1 NI-MMSI MUS musculus cDNA clone IMAGE:5661422 5' similar to TR:054788 054788
                                                                      CAD PROTEIN. ;, mRNA sequence.
BI789500
Mus musculus
                                                       BI789500.1
                   nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGTGAGTGACATCACACGTTTCCTCAGTGTGTTTAATGAGCCACATGCCGGCGTCATC
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Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
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Matches:
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Mismatches:
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Carden

Bennett, J., carc-

Cardenas

Gibbons, M.,

Eukaryota; Metazoa;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

nmalia; Eutheria; (bases 1 to 537)

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No.:
159 ATGCCCGGTTCCCGGCTGTGCCTGTACGAAGATGGCACGGATTTTATTGACGACTGCTTC
                                                  41 GluArgGlySerArgLeuCysLeuTyrGluAspGlyThrGluLeuThrGluAspTyrPhe 60
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Location/Qualifiers
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information or
obtaining a clone please contact: Juliana Brown
(brown@fas harvard.edu)
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Endocrine Pancreas Consortium
Harvard University. Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000)
Contact: Douglas Melton, Klau
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//lab_host="DH10B"
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/clone="IMAGE:5661422"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1
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/strain="ICR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,M., Koya,S., Matsuyama,T., Hili,Y., Ito,M., Kawai,J., Konno,H., Kouda,Okazaki,Y., Okido,T., Saito,R., Sakai,K., Ohno,M., Sasaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Sahata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Szuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Szuki,H., Muramatsu,M. and Hayashizaki,Y. Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegsc.riken.go.jp,

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

watahiki, M., Yoneda, Y., Ishkawa, T., Ozawa, K., Tanaka, T., Matsuura

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Hayashizaki, Y.
                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 643)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,i
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BB628807 RIKEN full-length enriched, 16
musculus cDNA clone 9630035119 5', mRNA
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Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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/db_xref-"taxon:9913"
/clone_lib-"MARC 2BOV"
/tissue_type-"pooled"
/lab_host-"DH10B"
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Library made from pooled tissue from testis,
semitendonosus muscle, longissimus muscle, pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 TyrValSerAspileArgArgPheLeuSerAlaPheHisGluProGlnValGlyLeuIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ026619 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA174E05 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthytidae; Oryziinae; Oryzias

Beloniformes; Adrianichthytidae; Oryziinae; Oryzias

1 (bases 1 to 688)
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BJ026619
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST project in Takeda's lab
Unpublished (2001)
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172 c 178 g 205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryzias latipes"
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487.50
71.60%
55.56%
27.25%
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Matches:
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188 AGGCGA 183
                                  337 ArgGln 338
                                                                     248 ATGGCGGTGAGGGCCTCCAGCCACGCAGGGGGAGTGAAGAAGAAGGTCCAGGTGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        280 AspGlyArgGluValAspTrpGluTyrPheTyrGlyLeuLeuPheThrSerGluAsnLeu 299
                                                                                                                                                                                                                                                                             428 CACAGGATTGAGAAGAAGAGGACCGTCATTCCCACGCTGCTGGAGCTCCTAGAGACTCAC 369
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